

SEQUENCE LISTING

<110> Benjanin, Stephane
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 91.US5.DIV

<140>

<141> 2001-11-13

<150> US 09/924,340

<151> 2001-08-06

<150> PCT/IB01/01715

<151> 2001-08-06

<150> US 60/305,456

<151> 2001-07-13

<150> US 60/302,277

<151> 2001-06-29

<160> 112

<170> JPatent

<210> 1

<211> 2016

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..1434

<220>

<221> CDS

<222> 1435..1836

<220>

<221> 3'UTR

<222> 1837..2016

<220>

<221> polyA_signal

<222> 1965..1970

<220>

<221> polyA_site

<222> 2001..2016

<400> 1

aaggtctctc	tgcatgcata	caccaaggaa	aagccacatg	aggacataac	caggaagaga	60
gccatcacca	agaacccgaa	catgcggaca	ccctgatctc	ggacttctag	ccttcagaac	120
cgttgccaca	gttttgatga	tcatctctct	cccaaccaag	atgggtggaa	aagcaaaaac	180
gtggtgaatc	ttggagcaat	ccgacaaggc	atgaaacgct	tccaatttct	gttaaactgc	240
tgtgagccag	ggacaattcc	tgatgcctcc	atcctagcag	ctgccttgga	tctactatgc	300
ggcattcttc	tgattcattt	ttctccattt	gtgctgtttt	tctctgtgat	gtgaatccat	360
ccctatccat	tatgtcatgc	ctccatcttt	tgctgcttct	tcagattgca	ctgagccata	420
agaggaagcc	cctgtgggtg	ccagagcagc	cttgctcctg	gaatgtgctc	gttttgttca	480
ccgctgcaac	cgtggcaact	ggccagagtg	gatgaaaggg	caccacgtga	acatcaccaa	540

```

gaaaggactt tcccggggac gctctcccat tgtgggcaac aagcgaaacc agaagctgca 600
gtggaatgca gccaaagctct tctaccaatg gggagacaag gaaaaaaggt gaagaataaa 660
aggaaattca agaggaccaa gtttctgcta atttttagaca gagctgaaca taaacacaca 720
taaagagggt ccatatattc ctcttttctt aaagattact tggaataact gttacaattt 780
ccgttaataa ttcagctgaa tgtgtctacc aatgtgttta ccaactaagg caattggcgt 840
ccgattgaat gagctgtgcc acggggaaaag tgagagccca gccaacctgc tgggtctcat 900
ttacgatgaa gagaccaaga ggagacttag aaaggaggat gaggaggaag acttttttaga 960
tgacattcca ctttcaagtc aatacacagc tcactcttgc tttaaaagct gattatgggtg 1020
caagcaactt tcgggctgga aattctacag aagcttgtct tttccattct tgatgagagg 1080
caaagtcccc ggcaacaaat taactcagga gagaaaatgg ttttcctgaa aaaaacgata 1140
gcttaaatat ctacagaaaag accgtaattt ccacctattt tcaaataaaa tcgtgaaaaa 1200
cacatttgga ctagagctga aacaacttca ctgccctcaa aacagcaaga cagacatccc 1260
tcataaaatg aactgacaga atttttatag ctccaaatct agttcactgc catatacata 1320
gtctaaatct gattgaatag cagcgtagaa atcttgcgaa attacttccc atttctgttt 1380
tcgttaaaag gtactgtgaa ccctctctaa tgcggttgcc cctttgcctt gaag atg 1437
Met
1
gca gca tgt cag ctt ctt ctg gag att acc acc ttc ctg cga gag acc 1485
Ala Ala Cys Gln Leu Leu Leu Glu Ile Thr Thr Phe Leu Arg Glu Thr
5 10 15
ttt tct tgc ctg ccc aga cct cgc act gag cct ctg gtg gct tca acg 1533
Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser Thr
20 25 30
gac cac acc aaa atg cca tct caa atg gaa cac gcc atg gaa acc atg 1581
Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met
35 40 45
atg ttt aca ttt cac aaa ttc gct ggg gat aaa ggc tac tta aca aag 1629
Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr Lys
50 55 60 65
gag gac ctg aga gta ctc atg gaa aag gag ttc cct gga ttt ttg gaa 1677
Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu Glu
70 75 80
aat caa aaa gac cct ctg gct gtg gac aaa ata atg aag gac ctg gac 1725
Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp
85 90 95
cag tgt aga gat ggc aaa gtg ggc ttc cag agc ttc ttt tcc cta att 1773
Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu Ile
100 105 110
gcg ggc ctc acc att gca tgc aat gac tat ttt gta gta cac atg aag 1821
Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys
115 120 125
cag aag gga aag aag taggcagaaa tgagcagttc gctcctccct gataagagtt 1876
Gln Lys Gly Lys Lys
130
gtcccaaagg gtcgcttaag gaatctgccc cacagcttcc cccatagaag gatttcatga 1936
gcagatcagg acacttagca aatgtaaaaa taaaatctaa ctctcatttg acaagcagag 1996
aaagaaaaaa aaaaaaaaaat 2016

```

<210> 2
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Ala Cys Gln Leu Leu Leu Glu Ile Thr Thr Phe Leu Arg Glu
 1 5 10 15
 Thr Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser
 20 25 30
 Thr Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr
 35 40 45
 Met Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr
 50 55 60
 Lys Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

120		125		130	
Phe Tyr Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile					
135		140		145	150
Gly Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn					
	155		160		165
Phe Ala Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser					
	170		175		180
Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp					
	185		190		195
Lys Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala					
	200		205		210
Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala					
215		220		225	230
Glu Met Ile Ile Glu Gln Val Lys Arg Gly Asn Thr Gln Arg Leu Ala					
	235		240		245
Cys Leu Ala Phe Ser Gly Gly Tyr Arg Ala His Gly Trp Cys Cys Gln					
	250		255		260
Thr Trp Ser Leu His					
265					

<210> 5
 <211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..83
 <220>
 <221> CDS
 <222> 84..317

<220>
 <221> 3'UTR
 <222> 318..438
 <220>
 <221> polyA_signal
 <222> 397..402

<220>
 <221> polyA_site
 <222> 423..438

<400> 5
 atagaaaagg acatctcttg agacttcact tcagcttcac tgacttcttg actctctct 60
 tgagtaaaag gactcagcca act atg aag ttt ttt gtc ttt gct tta gtc ttg 113
 Met Lys Phe Phe Val Phe Ala Leu Val Leu
 -15 -10
 gct ctc atg att tcc atg att agc gct gat tca cat gaa aag aga cat 161
 Ala Leu Met Ile Ser Met Ile Ser Ala Asp Ser His Glu Lys Arg His
 -5 1 5
 cat ggg tat aga aga aaa ttc cat gaa aag cat cat tca tac cat atc 209
 His Gly Tyr Arg Arg Lys Phe His Glu Lys His His Ser Tyr His Ile
 10 15 20
 aca cta cta cca ctt ttt gaa gaa tca tca aag agc aat gca aat gaa 257
 Thr Leu Leu Pro Leu Phe Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu
 25 30 35 40
 aaa cac tat aat tta ctg tat act ctt tgt ttc agg ata ctt gcc ttt 305
 Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe
 45 50 55
 tca att gtc act tgatgatata attgcaattt aaactgttaa gctgtgttca 357

Ser Ile Val Thr

60

gtactgtttc tgaataatag aaatcacttc tctaaaagca ataaatttca agcacatttt 417
taaataaaaa aaaaaaaaaa a 438

<210> 6

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..19

<400> 6

Met Lys Phe Phe Val Phe Ala Leu Val Leu Ala Leu Met Ile Ser Met
-15 -10 -5
Ile Ser Ala Asp Ser His Glu Lys Arg His His Gly Tyr Arg Arg Lys
1 5 10
Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe
15 20 25
Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu Lys His Tyr Asn Leu Leu
30 35 40 45
Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe Ser Ile Val Thr
50 55

<210> 7

<211> 968

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..31

<220>

<221> CDS

<222> 32..748

<220>

<221> 3'UTR

<222> 749..968

<220>

<221> polyA_signal

<222> 928..933

<220>

<221> polyA_site

<222> 953..968

<400> 7

tgatcaggac tcctcagttc accttctcac a atg agg ctc cct gct cag ctc 52
Met Arg Leu Pro Ala Gln Leu
-15
ctg ggg ctg cta atg ctc tgg gtc tct gga tcc agt ggg gat att gtg 100
Leu Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
-10 -5 1
atg act cag tct cca ctc ttc ctg ccc gtc acc cct gga gag ccg gcc 148
Met Thr Gln Ser Pro Leu Phe Leu Pro Val Thr Pro Gly Glu Pro Ala
5 10 15 20
tcc atc tcc tgc agg tct agt cag agc ctc ctg cat gtt caa ggg tcc 196
Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Val Gln Gly Ser

														25			30				35			
aac	tat	ttg	gat	tgg	tac	cac	cag	aag	cca	ggg	cag	tct	cca	caa	ctc	244								
Asn	Tyr	Leu	Asp	Trp	Tyr	His	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Gln	Leu									
				40					45					50										
ctg	ata	tac	ttg	ggg	tct	aat	cgg	gcc	tcc	ggg	gtc	cct	gac	agg	ttc	292								
Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg	Ala	Ser	Gly	Val	Pro	Asp	Arg	Phe									
				55					60					65										
agt	ggc	agt	gga	tca	ggc	aca	gat	ttc	aca	ctg	aaa	atc	agt	aga	gtg	340								
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val									
				70					75					80										
gag	gct	gag	gat	gtt	ggg	gtt	tat	tac	tgc	atg	caa	gct	cta	caa	act	388								
Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Ala	Leu	Gln	Thr									
85					90					95					100									
cca	ttc	act	ttc	ggc	cct	ggg	acc	aga	gtg	gat	atc	aag	cga	act	gtg	436								
Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr	Arg	Val	Asp	Ile	Lys	Arg	Thr	Val									
				105					110					115										
gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	cag	ttg	aaa	484								
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys									
				120					125					130										
tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	tat	ccc	aga	532								
Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg									
				135					140					145										
gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	aac	gcc	ctc	caa	tcg	ggg	aac	580								
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn									
				150					155					160										
tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc	tac	agc	628								
Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser									
				165					170					175										
ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	aaa	cac	aaa	676								
Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys									
				185					190					195										
gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc	gtc	aca	724								
Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr									
				200					205					210										
aag	agc	ttc	aac	agg	gga	gag	tgt	tagagggaga	agtgccccca	cctgctcctc	778													
Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys																	
				215					220															
agttccagcc tgacccccctc ccatacctttg gcctctgacc cttttttccac agggggaccta																838								
cccctattgc ggtcctccag ctcatctttc acctcacccc cctcctcctc cttggcttta																898								
aaaatgctaa tgttgaggga gaatgaataa ataaagtga tctttgcacc tgtaaaaaa																958								
aaaaaaaaa																968								

```
<210> 8
<211> 239
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> 1..20
```

<400>	8																
Met	Arg	Leu	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Met	Leu	Trp	Val	Ser		
-20					-15					-10					-5		
Gly	Ser	Ser	Gly	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Phe	Leu	Pro		
				1				5					10				
Val	Thr	Pro	Gly	Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser		
		15					20					25					
Leu	Leu	His	Val	Gln	Gly	Ser	Asn	Tyr	Leu	Asp	Trp	Tyr	His	Gln	Lys		
		30				35					40						
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg	Ala		
45					50					55					60		
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe		

tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
 tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
 ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggtg 694
 aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

<210> 12
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..14

<400> 12
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
 -10 -5 1
 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
 5 10 15
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 85 90

<210> 13
 <211> 732
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..253

<220>
 <221> CDS
 <222> 254..574

<220>
 <221> 3'UTR
 <222> 575..732

<400> 13
 agatgagtgt tcagctctca gcagagaggt tagctcctct ctgcagcttg tcctgttgct 60
 tcctcaagtc tggctgagtc cggagttttt atgagcctca gaggggagga agtgcattgct 120
 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgctggac ccacagcctg 180
 gccctcagga ctcaggcctt ccctggcttg aagattgggc ttcacctggg acctaccct 240
 tctgcctagg agc atg tct gcc tcc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5

```

aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
1 5 10 15
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
20 25 30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
35 40 45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
50 55 60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
65 70 75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
80 85 90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tgttatcagc 634
ctttgaaatg taggtagctt attatccaca ttttgcagat gaggaacag agtcaggtga 694
agtgctctttt ccaaggccaa gctcctgagg gcaggggc 732

```

```

<210> 14
<211> 107
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..14

```

```

<400> 14
Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
-10 -5 1
Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
5 10 15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
20 25 30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
35 40 45 50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
55 60 65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
70 75 80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
85 90

```

```

<210> 15
<211> 733
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..253

```

```

<220>
<221> CDS
<222> 254..574

```

```

<220>
<221> 3'UTR
<222> 575..733

```

<400> 15
 agatgagtgt tcagctctca gcagagaggt tagctctctt ctgcagcttg tcctgttgct 60
 tcctcaagtc tggctgagtc cggagttttt atgagcctca gaggggagga agtgcattgct 120
 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
 gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttacactggg acctaccctt 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
 tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
 ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggtg 694
 aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

<210> 16
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..14

<400> 16
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
 -10 -5 1
 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
 5 10 15
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 85 90

<210> 17
 <211> 1175
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR

<222> 1..326

<220>

<221> CDS

<222> 327..1013

<220>

<221> 3'UTR

<222> 1014..1175

<220>

<221> polyA_signal

<222> 1131..1136

<220>

<221> polyA_site

<222> 1160..1175

<400> 17

gaagcggagc ggtctaggga gccgcggccg cgggtcaccg gccgggtagc agttgctgag 60
tgtcagctag acagcagcga ctaggggctcg gccgcggcg agatgccttt gttcaccgcc 120
aacccttcg agcaagacgt ggtgatgccg attggtggaa aggagaaaat cacagaggaa 180
taggactttt cccatccaat tttgtaacaa ctaattttaa catagagact gaggcagcgg 240
ctgtggacaa attgaatgta attgatgatg atgtggagga aattaagaaa tcagagcctg 300
agcctgttta tatagatgag gataag atg gat aga gcc ctg cag gta ctt cag 353
Met Asp Arg Ala Leu Gln Val Leu Gln

1 5
agt ata gat cca aca gat tca aaa cca gac tcc caa gac ctt ttg gat 401
Ser Ile Asp Pro Thr Asp Ser Lys Pro Asp Ser Gln Asp Leu Leu Asp
10 15 20 25
tta gaa gat atc tgc caa cag atg ggt cca atg ata gat gaa aaa ctt 449
Leu Glu Asp Ile Cys Gln Gln Met Gly Pro Met Ile Asp Glu Lys Leu
30 35 40
gaa gaa att gat agg aag cat tca gaa ttg tct gaa ttg aat gtt aaa 497
Glu Glu Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys
45 50 55
gtc ctg gaa gct ctg gaa cta tat aac aaa ttg gtg aat gaa gca cca 545
Val Leu Glu Ala Leu Glu Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro
60 65 70
gtg tac tca gtc tat tca aag ctc cac cct cca gca cat tac cca cct 593
Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro
75 80 85
gca tca tct ggg gtt cca atg cag aca tat cca gtt caa tca cat ggt 641
Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly
90 95 100 105
gga aac tat atg ggt cag agc att cac caa gta act gtt gcc caa agc 689
Gly Asn Tyr Met Gly Gln Ser Ile His Gln Val Thr Val Ala Gln Ser
110 115 120
tat agc cta gga ccc gat caa att ggt cca ctg aga tct ctg cct cca 737
Tyr Ser Leu Gly Pro Asp Gln Ile Gly Pro Leu Arg Ser Leu Pro Pro
125 130 135
aat gtg aat tcc tca gtg aca gca cag cct gct caa act tca tat tta 785
Asn Val Asn Ser Ser Val Thr Ala Gln Pro Ala Gln Thr Ser Tyr Leu
140 145 150
agc act gga caa gac act gtt tcc aat cct act tat atg aac cag aac 833
Ser Thr Gly Gln Asp Thr Val Ser Asn Pro Thr Tyr Met Asn Gln Asn
155 160 165
tct aac cta cag tca gct act ggt aca act gct tac aca cag caa atg 881
Ser Asn Leu Gln Ser Ala Thr Gly Thr Thr Ala Tyr Thr Gln Gln Met
170 175 180 185
ggg atg tct gtg gat atg tca tct tat cag aac act act tcc aat ttg 929
Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu
190 195 200

```

cct caa ctg gca ggc ttt ccg gtg aca gtt cca gct cat cca gtt gca 977
Pro Gln Leu Ala Gly Phe Pro Val Thr Val Pro Ala His Pro Val Ala
      205                      210                      215
cag cag cac aca aat tac cat cag cag cct ctc ctt tagaaacaaa 1023
Gln Gln His Thr Asn Tyr His Gln Gln Pro Leu Leu
      220                      225
tcaagcattt tcttgaaagc cttcataagt gtattattca gtccttgtga taccaacctg 1083
aaaatattaa aacttttttc cctctcaact caaaaggacc atgaataaat aaagcacaaa 1143
aacctctctt attctgaaaa aaaaaaaaaa at 1175

```

```

<210> 18
<211> 229
<212> PRT
<213> Homo sapiens

```

```

<400> 18
Met Asp Arg Ala Leu Gln Val Leu Gln Ser Ile Asp Pro Thr Asp Ser
1      5      10      15
Lys Pro Asp Ser Gln Asp Leu Leu Asp Leu Glu Asp Ile Cys Gln Gln
      20      25      30
Met Gly Pro Met Ile Asp Glu Lys Leu Glu Glu Ile Asp Arg Lys His
      35      40      45
Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu
      50      55      60
Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys
      65      70      75      80
Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met
      85      90      95
Gln Thr Tyr Pro Val Gln Ser His Gly Gly Asn Tyr Met Gly Gln Ser
      100      105      110
Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln
      115      120      125
Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr
      130      135      140
Ala Gln Pro Ala Gln Thr Ser Tyr Leu Ser Thr Gly Gln Asp Thr Val
      145      150      155      160
Ser Asn Pro Thr Tyr Met Asn Gln Asn Ser Asn Leu Gln Ser Ala Thr
      165      170      175
Gly Thr Thr Ala Tyr Thr Gln Gln Met Gly Met Ser Val Asp Met Ser
      180      185      190
Ser Tyr Gln Asn Thr Thr Ser Asn Leu Pro Gln Leu Ala Gly Phe Pro
      195      200      205
Val Thr Val Pro Ala His Pro Val Ala Gln Gln His Thr Asn Tyr His
      210      215      220
Gln Gln Pro Leu Leu
225

```

```

<210> 19
<211> 844
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..111

```

```

<220>
<221> CDS
<222> 112..813

```

```

<220>
<221> 3'UTR
<222> 814..844

```

```

<400> 19
tttcctgttg cctgtctcta aacccctcca cattcccgcg gtccttcaga ctgcccggag 60
agcgcgctct gcctgccgcc tgcctgcctg ccactgaggg ttcccagcac c atg agg 117
                                         Met Arg
                                         -15
gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg gca gcc 165
Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala
-10 -5 1
cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa gaa act 213
Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr
5 10 15
gtg gca gag gtg act gag gta tct gtt gga gct aat cct gtc cag gtg 261
Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val
20 25 30
gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag gag gtg 309
Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Thr Glu Glu Glu Val
35 40 45 50
gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac ggc aag gtg 357
Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val
55 60 65
tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag gac ccc 405
Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro
70 75 80
acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc agc aat 453
Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn
85 90 95
gac aac aag acc ttc gac tct tcc tgc cac ttc ttt gcc aca aag tgc 501
Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys
100 105 110
acc ctg gag ggc acc aag aag ggc cac aag ctc cac ctg gac tac atc 549
Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile
115 120 125 130
ggg cct tgc aaa tac atc ccc cct tgc ctg gac tct gag ctg acc gaa 597
Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu
135 140 145
ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc acc ctg 645
Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu
150 155 160
tat gag agg gat gag gac aac aac ctt ctg act gag aag cag aag ctg 693
Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu
165 170 175
cgg gtg aag aag atc cat gag aat gag aag cgc ctg gag gca gga gac 741
Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp
180 185 190
cac ccc gtg gag ctg ctg gcc cgg gac tgc cag gct gtt tca gcc agg 789
His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg
195 200 205 210
aag gcc aaa atc aag agt gag atg tagaaagtgtg taaaatagaa aaagtggagt 843
Lys Ala Lys Ile Lys Ser Glu Met
215
t 844

```

```

<210> 20
<211> 234
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..17

```

```

<400> 20

```

Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 -15 -10 -5
 Ala Ala Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu
 1 5 10 15
 Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
 20 25 30
 Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
 35 40 45
 Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
 50 55 60
 Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
 65 70 75
 Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys
 80 85 90 95
 Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr
 100 105 110
 Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp
 115 120 125
 Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu
 130 135 140
 Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val
 145 150 155
 Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln
 160 165 170 175
 Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala
 180 185 190
 Gly Asp His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser
 195 200 205
 Ala Arg Lys Ala Lys Ile Lys Ser Glu Met
 210 215

<210> 21
 <211> 1997
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..126

<220>
 <221> CDS
 <222> 127..1020

<220>
 <221> 3'UTR
 <222> 1021..1997

<400> 21
 atcctctaag cttttaata ttgcttcgat ggtctgaatt tttatttcca gggaaaaaga 60
 gagttttgtc ccacagtcag caggccacta gtttattaac ttccagtcac cttgattttt 120
 gctaaa atg aag act ctg cag tct aca ctt ctg tta ctg ctt gtg 168
 Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Val
 -15 -10 -5
 cct ctg ata aag cca gca cca cca acc cag cag gac tca cgc att atc 216
 Pro Leu Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile
 1 5 10
 tat gat tat gga aca gat aat ttt gaa gaa tcc ata ttt agc caa gat 264
 Tyr Asp Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp
 15 20 25
 tat gag gat aaa tac ctg gat gga aaa aat att aag gaa aaa gaa act 312
 Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr
 30 35 40

[illegible][illegible][illegible][illegible][illegible][illegible][illegible]

<221> 3'UTR
<222> 1213..1746

<220>
<221> polyA_signal
<222> 1709..1714

<220>
<221> polyA_site
<222> 1733..1746

<400> 23
gcctcacca atg gtt ccc ttc atc tat ctg caa gcc cac ttt aca ctc tgt 51
Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys
-15 -10 -5
tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg 99
Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val
1 5 10
ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta 147
Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val
15 20 25 30
agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc 195
Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala
35 40 45
atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc 243
Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly
50 55 60
atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg 291
Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro
65 70 75
gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc 339
Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu
80 85 90
ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa 387
Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu
95 100 105 110
gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac 435
Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His
115 120 125
tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg 483
Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp
130 135 140
tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg 531
Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu
145 150 155
aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt 579
Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser
160 165 170
ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc 627
Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val
175 180 185 190
aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc 675
Lys Ser Ile Lys Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe
195 200 205
tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg 723
Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp
210 215 220
aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac 771
Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn
225 230 235
cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg 819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
240 245 250

<220>
 <221> UNSURE
 <222> 116
 <223> Xaa = Asn,Thr

<220>
 <221> UNSURE
 <222> 233
 <223> Xaa = Phe,Ser

<400> 28
 Met Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln
 1 5 10 15
 Gln Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe
 20 25 30
 Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg
 35 40 45
 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser
 50 55 60
 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val
 65 70 75 80
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg
 85 90 95
 Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn
 100 105 110
 Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn
 115 120 125
 Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile
 130 135 140
 Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn
 145 150 155 160
 Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu
 165 170 175
 Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu
 180 185 190
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp
 195 200 205
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser
 210 215 220
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr
 225 230 235 240
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr
 245 250 255
 Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile
 260 265 270
 Arg Pro Asn Asp Phe Ile Pro Asn Val Ile
 275 280

<210> 29
 <211> 1118
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..344

<220>
 <221> CDS
 <222> 345..1118

<220>
 <221> polyA_site

<222> 1103..1118

<400> 29

```
aatcctagtc ttcgtttggt ccggttgacac tcttctata gccagaggg cgagagggcc 60
tgtggcctgg ggaagaggg acgaggttct gcctggatcc cagcaggacg ctgtgccatt 120
tggaacaaa ggaatagtct gcctggaatc cctgcagatc ttggggccgg aggccagtcc 180
aacccttgga gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240
cggcccgag tagctgcaga ctccgcccgc gacgtgtgcg cgcttctctg ggccagagcg 300
agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356
                                Met Gly Arg Thr
cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
-15 -10 -5 1
tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
5 10 15
atc tgg gac gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500
Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val
20 25 30
gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
35 40 45
aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596
Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu
50 55 60 65
gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644
Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser
70 75 80
gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692
Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys
85 90 95
gaa cag gca agt gca aag gca ggc aaa ggg gct agg gtg ggt acc atc 740
Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile
100 105 110
tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788
Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg
115 120 125
ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836
Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg
130 135 140 145
gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884
Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala
150 155 160
cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat 932
Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr
165 170 175
aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980
Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn
180 185 190
atc ctg gag cga aca aat gat cct ttt att caa gaa gta gcc ttg gtc 1028
Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val
195 200 205
act ctg ggt aac aat gca gca tat tca ttt aac cag aat gcc ata cgt 1076
Thr Leu Gly Asn Asn Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg
210 215 220 225
gaa ttg ggt ggt gtc cca att att gca aaa aaa aaa aaa aaa 1118
Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys Lys Lys
230 235
```

<210> 30

<211> 258

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<220>
 <221> UNSURE
 <222> 49
 <223> Xaa = Glu, *

<400> 30
 Met Gly Arg Thr Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile
 -20 -15 -10 -5
 Gly Ala Gly Ala Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp
 1 5 10
 Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser
 15 20 25
 Xaa Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala
 30 35 40
 Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val
 45 50 55 60
 Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser
 65 70 75
 Gly Ser His Ser Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe
 80 85 90
 Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg
 95 100 105
 Val Gly Thr Ile Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys
 110 115 120
 Pro Gly Gly Arg Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg
 125 130 135 140
 Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys
 145 150 155
 Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe
 160 165 170
 Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln
 175 180 185
 Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu
 190 195 200
 Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln
 205 210 215 220
 Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys
 225 230 235
 Lys Lys

<210> 31
 <211> 1273
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..13

<220>
 <221> CDS
 <222> 14..1048

<220>
 <221> 3'UTR
 <222> 1049..1273

<220>

<221> polyA_signal

<222> 1234..1239

<220>

<221> polyA_site

<222> 1258..1273

<400> 31

```
agagggttggg aag atg gcg tgg cga ggc tgg gcg cag aga ggc tgg ggc      49
      Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly
      -25                                -20                                -15
tgc ggc cag gcg tgg ggt gcg tgc gtg ggc ggc cgc agc tgc gag gag      97
Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu
      -10                                -5                                1
ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac      145
Leu Thr Ala Val Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn
      5                                10                                15
ttc ttt att caa caa aaa tgc gga ttc aga aaa gca ccc agg aag gtt      193
Phe Phe Ile Gln Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val
      20                                25                                30                                35
gaa cct cga aga tca gac cca ggg aca agt ggt gaa gca tac aag aga      241
Glu Pro Arg Arg Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg
      40                                45                                50
agt gct ttg att cct cct gtg gaa gaa aca gtc ttt tat cct tct ccc      289
Ser Ala Leu Ile Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro
      55                                60                                65
tat cct ata agg agt ctc ata aaa cct tta ttt ttt act gtt ggg ttt      337
Tyr Pro Ile Arg Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe
      70                                75                                80
aca ggc tgt gca ttt gga tca gct gct att tgg caa tat gaa tca ctg      385
Thr Gly Cys Ala Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu
      85                                90                                95
aaa tcc agg gtc cag agt tat ttt gat ggt ata aaa gct gat tgg ttg      433
Lys Ser Arg Val Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu
      100                                105                                110                                115
gat agc ata aga cca caa aaa gaa gga gac ttc aga aag gag att aac      481
Asp Ser Ile Arg Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn
      120                                125                                130
aag tgg tgg aat aac cta agt gat ggc cag cgg act gtg aca ggt att      529
Lys Trp Trp Asn Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile
      135                                140                                145
ata gct gca aat gtc ctt gta ttc tgt tta tgg aga gta cct tct ctg      577
Ile Ala Ala Asn Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu
      150                                155                                160
cag cgg aca atg atc aga tat ttc aca tgc aat cca gcc tca aag gtc      625
Gln Arg Thr Met Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val
      165                                170                                175
ctt tgt tct cca atg ttg ctg tca aca ttc agt cat ttc tcc tta ttt      673
Leu Cys Ser Pro Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe
      180                                185                                190                                195
cac atg gca gca aat atg tat gtt ttg tgg agc ttc tct tcc agc ata      721
His Met Ala Ala Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile
      200                                205                                210
gtg aac att ctg ggt caa gag cag ttc atg gca gtg tac cta tct gca      769
Val Asn Ile Leu Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala
      215                                220                                225
ggt gtt att tcc aat ttt gtc agt tac gtg ggt aaa gtt gcc aca gga      817
Gly Val Ile Ser Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly
      230                                235                                240
aga tat gga cca tca ctt ggt gca gcc ctg aaa gcc att atc gcc atg      865
Arg Tyr Gly Pro Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met
      245                                250                                255
gat aca gca gga atg atc ctg gga tgg aaa ttt ttt gat cat gcg gca      913
```


265 270 275
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 280 285 290
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 295 300 305 310
 Gly Pro Lys Lys Gly Gly Ser Lys
 315

<210> 33
 <211> 723
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..72

<220>
 <221> CDS
 <222> 73..672

<220>
 <221> 3'UTR
 <222> 673..723

<220>
 <221> polyA_signal
 <222> 689..694

<220>
 <221> polyA_site
 <222> 708..723

<400> 33
 acaagaaaaag aacatggtct agactgaagt accaactaaa tcattctcctt tcaaattatc 60
 accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta 111
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val
 1 5 10
 ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159
 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser
 15 20 25
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg
 30 35 40 45
 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr
 50 55 60
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro
 65 70 75
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val
 80 85 90
 ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399
 Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr
 95 100 105
 aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447
 Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
 110 115 120 125
 ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495
 Leu Gly Ala Ile Ala Gly Ile Ile Leu Thr Phe Gly Phe Ile Leu
 130 135 140
 gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543

```

Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys
      145                      150                      155
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc 591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
      160                      165                      170
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc 639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
      175                      180                      185
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata 692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
      190                      195                      200
aagatgtgtt aaaataaaaa aaaaaaaaaa t 723

```

```

<210> 34
<211> 200
<212> PRT
<213> Homo sapiens

```

```

<400> 34
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
1      5      10      15
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
      20      25      30
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
      35      40      45
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
      50      55      60
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
65      70      75      80
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
      85      90      95
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
      100     105     110
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
      115     120     125
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
      130     135     140
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
145     150     155     160
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
      165     170     175
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
      180     185     190
Asp Cys Asp Cys Glu Gln Cys Cys
      195     200

```

```

<210> 35
<211> 845
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..118

```

```

<220>
<221> CDS
<222> 119..655

```

```

<220>
<221> 3'UTR
<222> 656..845

```

<220>
 <221> polyA_signal
 <222> 809..814

<220>
 <221> polyA_site
 <222> 830..845

<400> 35
 acaaatagcc cccgatatct gtgttaccag ccttgtctcg gccacctcaa ggataatcac 60
 taaattctgc caaaaggact gaggaacggg gcttggaataa gggcaagaat atcacggc 118
 atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
 Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
 1 5 10 15
 aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214
 Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
 20 25 30
 tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262
 Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
 35 40 45
 tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
 Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
 50 55 60
 gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358
 Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
 65 70 75 80
 ctg ctt atg tcg ttc atc ctg ctg ctg att atc ctc ctt gct gag 406
 Leu Leu Met Ser Phe Phe Ile Leu Leu Ile Ile Leu Leu Ala Glu
 85 90 95
 gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454
 Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
 100 105 110
 atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
 Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
 115 120 125
 atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
 Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
 130 135 140
 acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
 Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
 145 150 155 160
 tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
 Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
 165 170 175
 ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695
 Gly Pro Tyr
 atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggg 755
 attatctctc tatcagataa gattttgtta atgtactatt ttactcttca ataaataaaa 815
 cagtttatta tcgcaaaaaa aaaaaaaaaa 845

<210> 36
 <211> 179
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
 1 5 10 15
 Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
 20 25 30
 Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
 35 40 45
 Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met

<400> 38
 Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val
 1 5 10 15
 Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala
 20 25 30
 Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala
 35 40 45
 Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu
 50 55 60
 Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
 65 70 75 80
 Ala

<210> 39
 <211> 1816
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..259

<220>
 <221> CDS
 <222> 260..1048

<220>
 <221> 3'UTR
 <222> 1049..1816

<220>
 <221> polyA_signal
 <222> 1782..1787

<220>
 <221> polyA_site
 <222> 1801..1816

<400> 39
 actctggggc cattgccagc cggctgtagg cattcagggc agtgtcttct gcatctccta 60
 ggaacctcgg gaggcgcagc tccggcgccct ggtagcgaga ggcgggttcc ggagatcccc 120
 gcctcacttc gtccactgt ggtaggggt gagtctcgcg aatgttaagt gatttgctca 180
 aggtgcccac ttgcaggaa ttggagccca ggccagttct ctgagcctat cattagggct 240
 aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu
 -15 -10
 ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg 340
 Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp
 -5 1 5
 atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388
 Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met
 10 15 20
 ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat 436
 Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr
 25 30 35 40
 gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tgc tgg gtg ggg ccc 484
 Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro
 45 50 55
 aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc 532
 Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe
 60 70
 gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat 580
 Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His

Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys
45 50 55 60
Leu Leu His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val
65 70 75
Gly Leu Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn
80 85 90
Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe
95 100 105
Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala
110 115 120
Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly
125 130 135 140
Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn
145 150 155
Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser
160 165 170
Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val
175 180 185
Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys
190 195 200
Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Leu Leu Leu Gln Leu
205 210 215 220
Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr Val Ser Val Thr Gly
225 230 235
Arg Gln Pro Tyr Lys Ser Trp
240

<210> 41
<211> 643
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..90

<220>
<221> CDS
<222> 91..462

<220>
<221> 3'UTR
<222> 463..643

<220>
<221> polyA_signal
<222> 607..612

<220>
<221> polyA_site
<222> 628..643

<400> 41
accctaccc cacgccccct cccgcgcgcg cgggttaaact cccgcacctg agcatcggct 60
cacacctgca cccgcgccgg gcatagcacc atg cct gct tgt cgc cta ggc ccg 114
Met Pro Ala Cys Arg Leu Gly Pro
-25
cta gcc gcc gcc ctc ctc ctc agc ctg ctg ctg ttc ggc ttc acc cta 162
Leu Ala Ala Ala Leu Leu Leu Ser Leu Leu Leu Phe Gly Phe Thr Leu
-20 -15 -10
gtc tca ggc aca gga gca gag aag act ggc gtg tgc ccc gag ctc cag 210
Val Ser Gly Thr Gly Ala Glu Lys Thr Gly Val Cys Pro Glu Leu Gln
-5 1 5 10


```

gct gac cag aac tgc acg caa gag tgc gtc tcg gac agc gaa tgc gcc 258
Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala
      15      20      25
gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306
Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu
      30      35      40
ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354
Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro
      45      50      55
cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402
Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro
      60      65      70      75
ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450
Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val
      80      85      90
act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502
Thr Pro Asn Phe
      95
agttttctgcc tggccctgca tctgggtcca gccacctgc cctccccttt ttcgggactc 562
tgtattccct cttgggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622
tcagcaaaaa aaaaaaaaaa a 643

```

```

<210> 42
<211> 124
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..30

```

```

<400> 42
Met Pro Ala Cys Arg Leu Gly Pro Leu Ala Ala Ala Leu Leu Leu Ser
-30      -25      -20      -15
Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys
      -10      -5      1
Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu
      5      10      15
Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala
      20      25      30
Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys
      35      40      45      50
Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln
      55      60      65
Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn
      70      75      80
Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe
      85      90

```

```

<210> 43
<211> 501
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..227

```

```

<220>
<221> CDS
<222> 228..501

```

```

<400> 43

```

actcttactc tttctctctc actctctctc ttttcccacc ctttaagccaa gtacagggat 60
agttgtctca tcattggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120
ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
ccatggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236
Met Gln Gly
-30
act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
-25 -20 -15
aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
-10 -5 1
aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
5 10 15
cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
20 25 30 35
gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
40 45 50
gtt cct ttc tcc gaa ctg aaa gac a 501
Val Pro Phe Ser Glu Leu Lys Asp
55

<210> 44
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..33

<400> 44
Met Gln Gly Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val
-30 -25 -20
Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu
-15 -10 -5
Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
1 5 10 15
Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
20 25 30
Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
35 40 45
Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
50 55

<210> 45
<211> 960
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..97

<220>
<221> CDS
<222> 98..934

<220>
<221> 3'UTR

<222> 935..960

<400> 45

ataatcacct ctcattccag actatgtag gtcttaatgg tgggaggacg cccgagtgt 60
cggcccgttt caccgccagg aggaaggaca ctgggtc atg acg cca tca gaa ggc 115
Met Thr Pro Ser Glu Gly
1 5
gcc aga gca ggg acc gga cgc gag ttg gag atg ttg gac tcg ctg ttg 163
Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu Met Leu Asp Ser Leu Leu
10 15 20
gcc ttg ggc ggc ctg gtg ctg ctt cgg gat tcc gtg gag tgg gag ggg 211
Ala Leu Gly Gly Leu Val Leu Leu Arg Asp Ser Val Glu Trp Glu Gly
25 30 35
cgc agt ctc ttg aag gcg ctt gtc aag aaa tct gca ctg tgt ggg gag 259
Arg Ser Leu Leu Lys Ala Leu Val Lys Lys Ser Ala Leu Cys Gly Glu
40 45 50
caa gtg cat atc ctg ggc tgt gaa gtg agc gag gaa gag ttt cgt gaa 307
Gln Val His Ile Leu Gly Cys Glu Val Ser Glu Glu Glu Phe Arg Glu
55 60 65 70
ggg ttt gac tct gat atc aac aat cgg ctg gtt tac cat gac ttc ttc 355
Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu Val Tyr His Asp Phe Phe
75 80 85
aga gac cct ctc aac tgg tca aaa act gag gag gcc ttt cct ggg ggg 403
Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu Glu Ala Phe Pro Gly Gly
90 95 100
ccg ctg gga gcc ttg aga gcc atg tgc aag agg aca gat cct gtt cct 451
Pro Leu Gly Ala Leu Arg Ala Met Cys Lys Arg Thr Asp Pro Val Pro
105 110 115
gtc acc att gct ctc gat tca ctc agc tgg ctg cta ctt cgc ctt ccc 499
Val Thr Ile Ala Leu Asp Ser Leu Ser Trp Leu Leu Leu Arg Leu Pro
120 125 130
tgc acc aca ctc tgc cag gtc ctg cat gct gtg agc cat cag gac tct 547
Cys Thr Thr Leu Cys Gln Val Leu His Ala Val Ser His Gln Asp Ser
135 140 145 150
tgt cct ggt gac agc tcc tca gtg ggg aaa gtg agt gtg ctg ggc ttg 595
Cys Pro Gly Asp Ser Ser Val Gly Lys Val Ser Val Leu Gly Leu
155 160 165
cta cat gaa gag ctt cat gga cca ggc cct gtg gga gct ctc agc agc 643
Leu His Glu Glu Leu His Gly Pro Gly Pro Val Gly Ala Leu Ser Ser
170 175 180
ctt gct cag act gag gtg acc ctg ggc ggt acc atg ggc cag gcc tcg 691
Leu Ala Gln Thr Glu Val Thr Leu Gly Gly Thr Met Gly Gln Ala Ser
185 190 195
gcc cac atc ctg tgt cgg agg ccc cga cag cgc cca act gac cag act 739
Ala His Ile Leu Cys Arg Arg Pro Arg Gln Arg Pro Thr Asp Gln Thr
200 205 210
cag tgg ttc tcc atc ctt ccg gac ttc agc ctg gat ctc caa gag ggg 787
Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser Leu Asp Leu Gln Glu Gly
215 220 225 230
ccc tct gta gag tcc cag ccc tac tcc gat cct cat ata ccc ccg gta 835
Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp Pro His Ile Pro Val
235 240 245
tct aag aat gcc aag gcc aga aca agg aaa tgt agt tta gta tct ggt 883
Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys Cys Ser Leu Val Ser Gly
250 255 260
cac ggg aga gaa aat aaa agc tgc aga ggt tgg ggg tgg ggt cag gga 931
His Gly Arg Glu Asn Lys Ser Cys Arg Gly Trp Gly Trp Gly Gln Gly
265 270 275
ttc tagggatggg gcagagtggc agcatc 960
Phe

<210> 46

<211> 279

<212> PRT
 <213> Homo sapiens

<400> 46

```

Met Thr Pro Ser Glu Gly Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu
1          5          10          15
Met Leu Asp Ser Leu Leu Ala Leu Gly Gly Leu Val Leu Leu Arg Asp
          20          25          30
Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys
          35          40          45
Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser
          50          55          60
Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu
65          70          75          80
Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu
          85          90          95
Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys
          100         105         110
Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp
          115         120         125
Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala
          130         135         140
Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Ser Val Gly Lys
145          150         155         160
Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro
          165         170         175
Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly
          180         185         190
Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln
          195         200         205
Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser
          210         215         220
Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp
225          230         235         240
Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys
          245         250         255
Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly
          260         265         270
Trp Gly Trp Gly Gln Gly Phe
          275

```

<210> 47
 <211> 1294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..266

<220>
 <221> CDS
 <222> 267..1139

<220>
 <221> 3'UTR
 <222> 1140..1294

<220>
 <221> polyA_signal
 <222> 1246..1251

<220>

<221> polyA_site
<222> 1279..1294

<400> 47

```

gactctgagg ctcctctctt gctctaacag acagcagcga ctttaggctg gataatagtc 60
aaattcttac ctcgctcttt cactgctagt aagatcagat tgcgtttctt tcagttactc 120
ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180
ttcaatacct ggaaggaaaa acaaaataac ctcaactccg ttttgaaaaa aacattccaa 240
gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293
                                Met Ile Tyr Thr Met Lys Lys Val His
                                -25                                -20

gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341
Ala Leu Trp Ala Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro
                                -15                                -10                                -5

ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389
Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
                                1                                5                                10

acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437
Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
15                                20                                25                                30

gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat 485
Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
35                                40                                45

att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533
Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
50                                55                                60

aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581
Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
65                                70                                75

aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629
Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys
80                                85                                90

cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677
Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys
95                                100                                105                                110

gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725
Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu
115                                120                                125

aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773
Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe
130                                135                                140

cag gtg gat aat tat gga acc cag ctg aat gct gtg aat aac tcc ctg 821
Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu
145                                150                                155

act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc 869
Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro
160                                165                                170

tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag 917
Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu
175                                180                                185                                190

aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag 965
Asn Arg Phe Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys
195                                200                                205

tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa 1013
Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu
210                                215                                220

tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga 1061
Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly
225                                230                                235

ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata 1109
Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys Lys Gln Arg Val Lys Ile
240                                245                                250

gca tat gaa gaa att ttt gtt aaa aat atg tgaatttggt atagcaatgt 1159

```

Ala Tyr Glu Glu Ile Phe Val Lys Asn Met

255

260

aacattaatt ctactaaata ttttatatga aatgtttcac tatgattttc tatttttctt 1219

ctaaaatgct ttttaattaat atgttcatta aattttctat gcttattgta cttgttacca 1279

aaaaaaaaaaaa

1294

<210> 48

<211> 291

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..28

<400> 48

Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys

-25

-20

-15

Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu

-10

-5

1

Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys

5

10

15

20

Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys

25

30

35

Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu

40

45

50

Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser

55

60

65

Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys

70

75

80

Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr

85

90

95

100

Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly

105

110

115

Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn

120

125

130

Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr

135

140

145

Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val

150

155

160

Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala

165

170

175

180

Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser

185

190

195

Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn

200

205

210

Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys

215

220

225

Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg

230

235

240

Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val

245

250

255

260

Lys Asn Met

<210> 49

<211> 1194

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..47

<220>
 <221> CDS
 <222> 48..1100

<220>
 <221> 3'UTR
 <222> 1101..1194

<220>
 <221> polyA_signal
 <222> 1159..1164

<220>
 <221> polyA_site
 <222> 1179..1194

<400> 49
 ctccctcagct tcaggcacca ccactgacct gggacagtga atcgaca atg ccg tct 56
 Met Pro Ser
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
 -20 -15 -10 -5
 cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag 152
 Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
 1 5 10
 ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa 200
 Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
 15 20 25
 ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc 248
 Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
 30 35 40
 cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta 296
 Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu
 45 50 55 60
 gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc 344
 Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala
 65 70 75
 ttc act gtc aac ttc ggc gac acc gaa gag gcc aag aaa cag atc aac 392
 Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn
 80 85 90
 gat tac gtg gag aag ggt act caa ggc aaa att gtg gat ttg gtc aag 440
 Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys
 95 100 105
 gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt 488
 Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe
 110 115 120
 aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag 536
 Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu
 125 130 135 140
 gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag 584
 Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys
 145 150 155
 cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg 632
 Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp
 160 165 170
 gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg 680
 Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu
 175 180 185
 cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat 728
 Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp
 190 195 200
 atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta 776
 Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu

Thr	His	Asp	Ile	Ile	Thr	Lys	Phe	Leu	Glu	Asn	Glu	Asp	Arg	Arg	Ser
				205					210					215	
Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp	Leu
				220				225					230		
Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn	Gly
				235			240					245			
Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser	Lys
	250					255					260				
Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu	Ala
265					270				275						280
Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile	Pro	Met	Ser	Ile	Pro	Pro	Glu
				285				290					295		
Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Asp	Gln	Asn	Thr
			300					305					310		
Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys	
		315					320					325			

<210> 51
 <211> 1317
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..289

<220>
 <221> CDS
 <222> 290..1162

<220>
 <221> 3'UTR
 <222> 1163..1317

<220>
 <221> polyA_signal
 <222> 1269..1274

<220>
 <221> polyA_site
 <222> 1302..1317

<400> 51
 aactgccagt gatctctgaa gccgactctg aggctccctc tttgctctaa cagacagcag 60
 cgacttttag ctggataata gtcaaattct tacctcgctc tttcactgct agtaagatca 120
 gattgcgttt ctttcagtta ctcttcaatc gccagtttct tgatctgctt ctaaaagaag 180
 aagtagagaa gataaatcct gtcttcaata cctggaagga aaaacaaaat aacctcaact 240
 ccgttttgaa aaaaacattc caagaacttt catcagagat tttacttag atg att tac 298
 Met Ile Tyr
 -25
 aca atg aag aaa gta cat gca ctt tgg gct tct gta tgc ctg ctg ctt 346
 Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys Leu Leu Leu
 -20 -15 -10
 aat ctt gcc cct gcc cct ctt aat gct gat tct gag gaa gat gaa gaa 394
 Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu
 -5 1 5
 cac aca att atc aca gat acg gag ttg cca cca ctg aaa ctt atg cat 442
 His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys Leu Met His
 10 15 20
 tca ttt tgt gca ttc aag tcg gat gat ggc cca tgt aaa gca atc atg 490
 Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys Ala Ile Met
 25 30 35 40
 aaa aga ttt ttc ttc aat att ttc act cga cag tgc gaa gaa ttt ata 538

Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile
45 50 55
tat ggg gga tgt gaa gga aat cag aat cga ttt gaa agt ctg gaa gag 586
Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu
60 65 70
tgc aaa aaa atg tgt aca aga gaa aag cca gat ttc tgc ttt ttg gaa 634
Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu
75 80 85
gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat aac 682
Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
90 95 100
aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga tgc ctg ggc 730
Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
105 110 115 120
aat atg aac aat ttt gag aca ctg gaa gaa tgc aag aac att tgt gaa 778
Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu
125 130 135
gat ggt ccg aat ggt ttc cag gtg gat aat tat gga acc cag ctc aat 826
Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn
140 145 150
gct gtg aat aac tcc ctg act ccg caa tca acc aag gtt ccc agc ctt 874
Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu
155 160 165
ttt gaa ttt cac ggt ccc tca tgg tgt ctc act cca gca gac aga gga 922
Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly
170 175 180
ttg tgt cgt gcc aat gag aac aga ttc tac tac aat tca gtc att ggg 970
Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly
185 190 195 200
aaa tgc cgc cca ttt aag tac agt gga tgt ggg gga aat gaa aac aat 1018
Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn
205 210 215
ttt act tcc aaa caa gaa tgt ctg agg gca tgt aaa aaa ggt ttc atc 1066
Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile
220 225 230
caa aga ata tca aaa gga ggc cta att aaa acc aaa aga aaa aga aag 1114
Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys
235 240 245
aag cag aga gtg aaa ata gca tat gaa gaa att ttt gtt aaa aat atg 1162
Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
250 255 260
tgaatttggt atagcaatgt aacattaatt ctactaaata ttttatatga aatggtttcac 1222
tatgattttc tattttttctt ctaaaatgct tttaattaat atgttcatta aattttctat 1282
gcttattgta cttgttatca aaaaaaaaaa aaaaa 1317

<210> 52
<211> 291
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..28

<400> 52
Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
-25 -20 -15
Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
-10 -5 1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5 10 15 20
Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys
25 30 35

180 185 190
 Ser Phe Arg Ile His Phe Trp Gly Cys
 195 200

<210> 57
 <211> 1133
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..475

<220>
 <221> CDS
 <222> 476..964

<220>
 <221> 3'UTR
 <222> 965..1133

<220>
 <221> polyA_signal
 <222> 1101..1106

<220>
 <221> polyA_site
 <222> 1118..1133

<400> 57
 gacataatca gagctatgct ggaggagaag agggcagcca ttgctggct ggcttgagct 60
 gagccaggag gtggcaggac gagttaggag gctggttcag tagctcgggc aagagcaggg 120
 cccccagga tctgaaggcc tcccaggccc cccaggccca gcgggtccca gaggagagcg 180
 aggaccccaa ggtaactccg gtgagaaggc cgaccaggga tttcaaggcc agccaggctt 240
 tccgggcccc cccgggtcccc ctggattccc aggcaaagtt ggatcacctg gcccacctgg 300
 cccctcaagca gagaaggcca gcgaagggat tcgaggccca tcaggcctgc ctggctcccc 360
 tggggccaccg ggacctcctg ggattcaggc ccccgccggc ctggatgggt tggatgggaa 420
 ggatggcaag cctggcctga ggggggaccc tggctcctgct ggccccctg gactc atg 478
 Met
 1
 gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526
 Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly
 5 10 15
 cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574
 Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg
 20 25 30
 cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622
 Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro
 35 40 45
 ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670
 Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly
 50 55 60 65
 cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718
 Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
 70 75 80
 gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766
 Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly
 85 90 95
 cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814
 Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
 100 105 110
 ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862
 Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly

```

      115              120              125
cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc 910
Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
130              135              140              145
atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct 958
Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
      150              155              160
ttt ggc tgaaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg 1014
Phe Gly
ccaaagctta taggactctg tgacagggtg tgaatgtttt tttgttggtt gttgttggtt 1074
ttaattgctg ttaatatattt ttaaataata aagaaacaaa actaaaaaaaa aaaaaaaaaa 1133

```

```

<210> 58
<211> 163
<212> PRT
<213> Homo sapiens

```

```

<400> 58
Met Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro
1              5              10              15
Gly Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly
      20              25              30
Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg
      35              40              45
Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro
      50              55              60
Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala
      65              70              75              80
Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro
      85              90              95
Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro
      100              105              110
Met Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met
      115              120              125
Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly
      130              135              140
Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly
      145              150              155              160
Pro Phe Gly

```

```

<210> 59
<211> 838
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..78

```

```

<220>
<221> CDS
<222> 79..642

```

```

<220>
<221> 3'UTR
<222> 643..838

```

```

<220>
<221> polyA_signal
<222> 799..804

```

```

<220>
<221> polyA_site

```


<222> 823..838

<400> 59

```
aaagactgcg tgcagaaggt gactgtctca gtggagctgg gtcattctcag gccttggtc 60
cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111
      Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met
      1          5          10
aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159
Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp
      15          20          25
aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tgc agc ctg 207
Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu
      30          35          40
gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255
Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
      45          50          55
gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa 303
Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
      60          65          70          75
gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat 351
Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
      80          85          90
gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag 399
Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
      95          100          105
gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447
Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp
      110          115          120
cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat 495
His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
      125          130          135
gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543
Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
      140          145          150          155
tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591
Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
      160          165          170
gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639
Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
      175          180          185
aaa tgaagatact gacaccacct ttgccctccc cgtcaccgcg caccaccct 692
Lys
gacctctccc tcagctgtcc tgtgccccgc cctctccccgc acactcagtc cccctgcctg 752
gcgttctctgc cgcagctctg acctggtgct gtcgccctgg catcttaata aamcctgctt 812
atatttcctt aaaaaaaaaa aaaaaa 838
```

<210> 60

<211> 188

<212> PRT

<213> Homo sapiens

<400> 60

```
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
1          5          10          15
Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala
      20          25          30
Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp
      35          40          45
Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
      50          55          60
Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
      65          70          75          80
Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala
```

				85					90					95			
Thr	Glu	Glu	Pro	Gly	Glu	Ser	Phe	Cys	Asp	Lys	Val	Met	Arg	Trp	Phe		
			100					105					110				
Gln	Ala	Met	Leu	Gln	Arg	Leu	Gln	Thr	Trp	Trp	His	Gly	Val	Leu	Ala		
		115					120					125					
Trp	Val	Lys	Glu	Lys	Val	Val	Ala	Leu	Val	His	Ala	Val	Gln	Ala	Leu		
	130					135					140						
Trp	Lys	Gln	Phe	Gln	Ser	Phe	Cys	Cys	Ser	Leu	Ser	Glu	Leu	Phe	Met		
145					150					155					160		
Ser	Ser	Phe	Gln	Ser	Tyr	Gly	Ala	Pro	Arg	Gly	Asp	Lys	Glu	Glu	Leu		
			165					170						175			
Thr	Pro	Gln	Lys	Cys	Ser	Glu	Pro	Gln	Ser	Ser	Lys						
			180					185									

<210> 61
 <211> 862
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..158

<220>
 <221> CDS
 <222> 159..764

<220>
 <221> 3'UTR
 <222> 765..862

<400> 61
 attttttttt ttggcacgcc tgcagccaag ttggggaggg tttcctggac agaggtcctt 60
 tggctgctgc cttaagacgt gcagcctggg ccgtggtgt cactgcgttc ggaccagac 120
 ccgctgcagg cagcagcagc ccccgccgc gcagcagc atg gag ctc tgg ggg gcc 176
 Met Glu Leu Trp Gly Ala
 -20 -15
 tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224
 Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Thr Glu
 -10 -5 1
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272
 Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val
 5 10 15
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320
 Val Asn Thr Lys Met Phe Glu Leu Lys Ser Arg Leu Asp Thr Leu
 20 25 30
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368
 Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val
 35 40 45 50
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
 55 60 65
 cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tcg cgc ggg 464
 Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly
 70 75 80
 ggc acc ctg agc acc cct cag act ggc tcg gag aac gac gcc ctg tat 512
 Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
 85 90 95
 gag tac ctg cgc cag agc gtg ggc aac gag gcc gag atc tgg ctg ggc 560
 Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
 100 105 110
 ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc 608
 Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala

```

115          120          125          130
cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
          135          140          145
ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
          150          155          160
aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
          165          170          175
ttc ggg atc gtg tagccggcgg ggcggggggc gtgggggggc tggaggaggg 804
Phe Gly Ile Val
          180
caggagccgc gggaggccgg gaggaggggtg gggaccttgc agcccccatc ctctccgt 862

```

```

<210> 62
<211> 202
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..21

```

```

<400> 62
Met Glu Leu Trp Gly Ala Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu
-20 -15 -10
Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val
-5 1 5 10
Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
15 20 25
Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
30 35 40
Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys
45 50 55
Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu
60 65 70 75
Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser
80 85 90
Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu
95 100 105
Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp
110 115 120
Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu
125 130 135
Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu
140 145 150 155
Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln
160 165 170
Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val
175 180

```

```

<210> 63
<211> 618
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..194

```

```

<220>
<221> CDS

```

<222> 195..587

<220>

<221> 3'UTR

<222> 588..618

<220>

<221> polyA_signal

<222> 578..583

<220>

<221> polyA_site

<222> 604..618

<400> 63

atttgcttag gtctgatcaa tctgctccac acaatttctc agtgatcctc tgcattctctg 60
cctacaagggt cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120
ttcggttttac cttgatctct ctctgacaaa gaaatccaga tgatgagaga cctgatgaag 180
acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230
Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu
-20 -15 -10
act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278
Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala
-5 1 5
cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326
Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln
10 15 20
agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374
Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala
25 30 35
tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422
Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr
40 45 50 55
aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470
Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser
60 65 70
atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518
Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg
75 80 85
act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566
Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met
90 95 100
tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618
Cys Phe Ala Leu Leu Asn Cys
105 110

<210> 64

<211> 131

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..22

<400> 64

Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
-20 -15 -10
Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
-5 1 5 10
Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
15 20 25
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln

<222> 1..62

<220>

<221> CDS

<222> 63..572

<220>

<221> 3'UTR

<222> 573..789

<220>

<221> polyA_signal

<222> 750..755

<220>

<221> polyA_site

<222> 774..789

<400> 67

```
atatgtcatc agggcccccg cctgggaggt gtgctgccag agattttgcc tcttcaaggt 60
ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
1 5 10 15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
20 25 30
gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
35 40 45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
50 55 60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
65 70 75
ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
80 85 90 95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
100 105 110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
115 120 125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
130 135 140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
145 150 155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
160 165 170
gaggagggac gcccagggtg gggaggaaga gtctgcaagc agggctgtgg agttagggtt 652
caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772
gaaaaaaaaa aaaaaaaa 789
```

<210> 68

<211> 170

<212> PRT

<213> Homo sapiens

ttg Leu	gag Glu	gga Gly	aat Asn	gaa Glu	atc Ile	tgt Cys	gat Asp	tgt Cys	ggg Gly	act Thr	gag Glu	gct Ala	caa Gln	tgt Cys	gga Gly	1308
385390395																
cct Pro	gca Ala	agc Ser	tgt Cys	tgt Cys	gat Asp	ttt Phe	cga Arg	act Thr	tgt Cys	gta Val	ctg Leu	aaa Lys	gac Asp	gga Gly	gca Ala	1356
400405410415																
aaa Lys	tgt Cys	tat Tyr	aaa Lys	gga Gly	ctg Leu	tgc Cys	tgc Cys	aaa Lys	gac Asp	tgt Cys	caa Gln	att Ile	tta Leu	caa Gln	tca Ser	1404
420425430																
ggc Gly	gtt Val	gaa Glu	tgt Cys	agg Arg	ccg Pro	aaa Lys	gca Ala	cat His	cct Pro	gaa Glu	tgt Cys	gac Asp	atc Ile	gct Ala	gaa Glu	1452
435440445																
aat Asn	tgt Cys	aat Asn	gga Gly	agc Ser	tca Ser	cca Pro	gaa Glu	tgt Cys	ggg Gly	cct Pro	gac Asp	ata Ile	act Thr	tta Leu	atc Ile	1500
450455460																
aat Asn	gga Gly	ctt Leu	tca Ser	tgc Cys	aaa Lys	aat Asn	aat Asn	aag Lys	ttt Phe	att Ile	tgt Cys	tat Tyr	gac Asp	gga Gly	gac Asp	1548
465470475																
tgc Cys	cat His	gat Asp	ctc Leu	gat Asp	gca Ala	cgt Arg	tgt Cys	gag Glu	agt Ser	gta Val	ttt Phe	gga Gly	aaa Lys	ggg Gly	tca Ser	1596
480485490495																
aga Arg	aat Asn	gct Ala	cca Pro	ttt Phe	gcc Ala	tgc Cys	tat Tyr	gaa Glu	gaa Glu	ata Ile	caa Gln	tct Ser	caa Gln	tca Ser	gac Asp	1644
500505510																
aga Arg	ttt Phe	ggg Gly	aac Asn	tgt Cys	ggg Gly	agg Arg	gat Asp	aga Arg	aat Asn	aac Asn	aaa Lys	tat Tyr	gtg Val	ttc Phe	tgt Cys	1692
515520525																
gga Gly	tgg Trp	agg Arg	aat Asn	ctt Leu	ata Ile	tgt Cys	gga Gly	aga Arg	tta Leu	gtt Val	tgt Cys	acc Thr	tac Tyr	cct Pro	act Thr	1740
530535540																
cga Arg	aag Lys	cct Pro	ttc Phe	cat His	caa Gln	gaa Glu	aat Asn	ggg Gly	gat Asp	gtg Val	att Ile	tat Tyr	gct Ala	ttc Phe	gta Val	1788
545550555																
cga Arg	gat Asp	tct Ser	gta Val	tgc Cys	ata Ile	acc Thr	gta Val	gac Asp	tac Tyr	aaa Lys	ttg Leu	cct Pro	cga Arg	aca Thr	gtt Val	1836
560565570575																
cca Pro	gat Asp	cca Pro	ctg Leu	gct Ala	gtc Val	aaa Lys	aat Asn	ggc Gly	tct Ser	cag Gln	tgt Cys	gat Asp	att Ile	ggg Gly	agg Arg	1884
580585590																
gtt Val	tgt Cys	gta Val	aat Asn	cgt Arg	gaa Glu	tgt Cys	gta Val	gaa Glu	tca Ser	agg Arg	ata Ile	att Ile	aag Lys	gct Ala	tca Ser	1932
595600605																
gca Ala	cat His	gtt Val	tgt Cys	tca Ser	caa Gln	cag Gln	tgt Cys	tct Ser	gga Gly	cat His	gga Gly	gtg Val	tgt Cys	gat Asp	tcc Ser	1980
610615620																
aga Arg	aac Asn	aag Lys	tgc Cys	cat His	tgt Cys	tcg Ser	cca Pro	ggc Gly	tat Tyr	aag Lys	cct Pro	cca Pro	aac Asn	tgc Cys	caa Gln	2028
625630635																
ata Ile	cgt Arg	tcc Ser	aaa Lys	gga Gly	ttt Phe	tcc Ser	ata Ile	ttt Phe	cct Pro	gag Glu	gaa Glu	gat Asp	atg Met	ggg Gly	tca Ser	2076
640645650655																
atc Ile	atg Met	gaa Glu	aga Arg	gca Ala	tct Ser	ggg Gly	aag Lys	act Thr	gaa Glu	aac Asn	acc Thr	tgg Trp	ctt Leu	cta Leu	ggg Gly	2124
660665670675																
ttc Phe	ctc Leu	att Ile	gct Ala	ctt Leu	cct Pro	att Ile	ctc Leu	att Ile	gta Val	aca Thr	acc Thr	gca Ala	ata Ile	gtt Val	ttg Leu	2172
680685690695																
gca Ala	agg Arg	aaa Lys	cag Gln	ttg Leu	aaa Lys	aac Asn	tgg Trp	ttc Phe	gcc Ala	aag Lys	gaa Glu	gag Glu	gaa Glu	ttc Phe	cca Pro	2220
700705710715																
agt Ser	agc Ser	gaa Glu	tct Ser	aaa Lys	tcg Ser	gaa Glu	ggg Gly	agc Ser	aca Thr	cag Gln	aca Thr	tat Tyr	gcc Ala			

```

tcc agc tca gaa ggc agc act cag aca tat gcc ggc caa acc aga tca 2316
Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser
720 725 730 735
gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt 2364
Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser
740 745 750
gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca 2412
Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr
755 760 765
caa agc agt agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc 2467
Gln Ser Ser Ser Asn
770
tcgctaagaa atgaaaattc tgtcttttcc tccgtgggtca cagctgaaag aaacaataaa 2527
ttgagtgtgg accaaaaaaa aaaaaaaat 2556

```

```

<210> 70
<211> 787
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..16

```

```

<400> 70
Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
-15 -10 -5
Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
1 5 10 15
Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
20 25 30
Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
35 40 45
Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn
50 55 60
Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
65 70 75 80
Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser
85 90 95
Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
100 105 110
Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His
115 120 125
Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
130 135 140
Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
145 150 155 160
Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
165 170 175
Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
180 185 190
Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
195 200 205
Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
210 215 220
Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
225 230 235 240
Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp
245 250 255
Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
260 265 270
Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
275 280 285

```


<210> 71
 <211> 1603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..7

<220>
 <221> CDS
 <222> 8..763

<220>
 <221> 3'UTR
 <222> 764..1603

<220>
 <221> polyA_signal
 <222> 1562..1567

<220>
 <221> polyA_site
 <222> 1588..1603

<400> 71
 gagaagg atg ggg ccg cat cta cac ctg tgc ctg tgt gtg cct gac ctg 49
 Met Gly Pro His Leu His Leu Cys Leu Cys Val Pro Asp Leu
 -15 -10 -5
 cgg tca ctc cgt gtc tgt gtg tcc ctc tgg tct gtc cac cac agg cca 97
 Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro
 1 5 10
 cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc 145
 His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu
 15 20 25 30
 ctg tac ctc tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata 193
 Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile
 35 40 45
 gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241
 Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val
 50 55 60
 cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289
 Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu
 65 70 75
 gga cag ctg gac cgg cct cca gac ctc gcc cat gac ggg agg agt ctg 337
 Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu
 80 85 90
 tgg ctg aac atc agg ggc aag gag gcg gct gcc cta tcc atg ttc cat 385
 Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Leu Ser Met Phe His
 95 100 105 110
 gtc tcc acg cca ctg cca gtg atg acc ggt ggt ttc ctg agc tgc atc 433
 Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile
 115 120 125
 ttg ggc ttg gtg ctg ccc ctg gcc tat ggc ttc cag cct gac ctg gtg 481
 Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val
 130 135 140
 ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gst gca 529
 Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala
 145 150 155
 ctc ctg gct gca atg ctt cgg ggg ctg gca ggg ggc cga gtc ctg gcc 577
 Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Arg Val Leu Ala
 160 165 170
 ctc ctg gag gag aac tcc aca ccc cag cta gca ggg atc ctg gcc cgg 625

Leu Leu Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg
 175 180 185 190
 gtg ctg aat gga gag gca cct cct agc cta ggc cct tcc tct gtg gcc 673
 Val Leu Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala
 195 200 205
 tcc cca gag gac gtc cag gcc ctg atg tac ctg aga ggg cag ctg gag 721
 Ser Pro Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu
 210 215 220
 cct cag tgg aag atg ttg cag tgc cat cct cac ctg gtg gct 763
 Pro Gln Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala
 225 230 235
 tgaatcggc caaggtggga gcatttacac cgcagaaatg acaccgcacg ccagcgcccc 823
 gcgcccgga tccggacccc aagcccacgg ctccctcgac tctggggcac ggaaccccg 883
 ccactccaa tccccgcgcc cggccctctc ccaccgtgc ttcccccgct ccaccctca 943
 cctcacctcg cccccgcccc acccatcgcg ccccgggcggc tgttattgtt cggctgggct 1003
 cggtcgggcg ctgtctccct cggtctcgcg ggtgtcagtt cgtccggctt cctcacagcc 1063
 cctactccc ggccggtgac agcagcagcg gcggcgccg gcggcgccg gcgtttcgag 1123
 gctgagcggc accgggggtg gggcgccggg gaggagcagc agcgggagga ggagccgtgt 1183
 gccctggcac tgagcgccg cgcccatggc gtacgcctat ctcttcaagt acatcataat 1243
 cggcgacaca ggtgttggt aatcatgctt attgtacag tttacagaca agaggttcag 1303
 ccagtgcag accttactat tgggtgtagag ttcgggtgctc gaatgataac tattgatggg 1363
 aaacagataa aacttcagat atgggatacg gcagggcaag aatcctttcg ttccatcaca 1423
 aggtcgtatt acagaggtgc agcaggagct ttactagttt acgatattac acggagagat 1483
 acattcaacc acttgacaac ctggttagaa gatgcccgcc agcattccaa ttccaacatg 1543
 gtcattatgc ttattggaaa taaaagtgat ttagaatcta gaagaaaaaa aaaaagaaaa 1603

<210> 72
 <211> 252
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17

<220>
 <221> UNSURE
 <222> 173
 <223> Xaa = Ala,Gly

<400> 72
 Met Gly Pro His Leu His Leu Cys Leu Cys Val Pro Asp Leu Arg Ser
 -15 -10 -5
 Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro His Glu
 1 5 10 15
 Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu Leu Tyr
 20 25 30
 Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile Ala Ala
 35 40 45
 Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val Arg Arg
 50 55 60
 Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu Gly Gln
 65 70 75
 Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu Trp Leu
 80 85 90 95
 Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His Val Ser
 100 105 110
 Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile Leu Gly
 115 120 125
 Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val Leu Val
 130 135 140
 Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala Leu Leu
 145 150 155

Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala Leu Leu
 160 165 170 175
 Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg Val Leu
 180 185 190
 Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala Ser Pro
 195 200 205
 Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu Pro Gln
 210 215 220
 Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala
 225 230 235

<210> 73
 <211> 879
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..8

<220>
 <221> CDS
 <222> 9..395

<220>
 <221> 3'UTR
 <222> 396..879

<220>
 <221> polyA_site
 <222> 864..879

<400> 73
 aggccaac atg gcc gtg ctg ctg ctg ctg ctc cgt gcc ctc cgc cgg ggt 50
 Met Ala Val Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly
 -15 -10 -5
 cca gcc ccg ggt cct cgg ccg ctg tgg gcc cca gcc ccg gcc tgg agt 98
 Pro Gly Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser
 1 5 10 15
 cca ggg ttc ccc gcc agg ccc ggg agg ggg cgg ccg tac atg gcc agc 146
 Pro Gly Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser
 20 25 30
 agg cct ccg ggg gac ctc gcc gag gct gga gcc cga gct ctg cag agc 194
 Arg Pro Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser
 35 40 45
 tta caa ttg aga ctg cta acc cct acc ttt gaa ggg atc aac gga ttg 242
 Leu Gln Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu
 50 55 60
 ttg ttg aaa caa cat tta gtt cag aat cca gtc aga ctc tgg caa ctt 290
 Leu Leu Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu
 65 70 75
 tta ggt ggt act ttc tat ttt aac acc tca agg ttg aag cag aag aat 338
 Leu Gly Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn
 80 85 90 95
 aag gag aag gat aag tcg aag ggg aag gcg cct gaa gag gac gaa ggt 386
 Lys Glu Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly
 100 105 110
 ata ttc atc tgatgttctt cagtcagtag ctgcctctgg atgtctttac 435
 Ile Phe Ile
 rttttctgttt wccttttagc aaggtgaaac cagtcctggam aatggggaga tgggccgggt 495
 gcagtggctc acacttgtaa tcgaaacgct ttgggaggcc caggtggaag gatcacttga 555
 ggccataacc acatagctag accctgtctc actgcaaatt aaaaggctgg gcgtgggtggc 615
 tcacacctgt aatcccagca ctttggggagg ctgaggcagg cggatcacct gcaccctggc 675

```

caacatgggtg aaaccccgtc ttactataaa atagaaaatt agccggggtg gatggcacac 735
gcctgtaatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctgggaggtg 795
gaggttgctg tgagtggaga tcatgccatt gcactccagc ctgagcaaca agagcaaac 855
tccatcccaa aaaaaaaaaa aaaa
879

```

```

<210> 74
<211> 129
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..16

```

```

<400> 74
Met Ala Val Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly Pro Gly
-15 -10 -5
Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser Pro Gly
1 5 10 15
Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro
20 25 30
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln
35 40 45
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
50 55 60
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
65 70 75 80
Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu
85 90 95
Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe
100 105 110
Ile

```

```

<210> 75
<211> 1634
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..87

```

```

<220>
<221> CDS
<222> 88..1269

```

```

<220>
<221> 3'UTR
<222> 1270..1634

```

```

<220>
<221> polyA_signal
<222> 1594..1599

```

```

<220>
<221> polyA_site
<222> 1619..1634

```

```

<400> 75
aaagttcctc agcccttggc tcctgcccag tgtttagggt gttggcggag acaaagggga 60
agagtcatcg cctgtcgggg ctaggat atg atg ggt gtg ttt gta gtt gct gct 114
Met Met Gly Val Phe Val Val Ala Ala
1 5

```



```

305          310          315          320
Ala Pro Gln Tyr Leu Ala Val Glu Arg Ser Leu Asp Leu Asp Ile Ser
          325          330          335
Lys Thr Asn Val Asn Gly Gly Ala Ile Ala Leu Gly His Pro Leu Gly
          340          345          350
Gly Ser Gly Ser Arg Ile Thr Ala His Leu Val His Glu Leu Arg Arg
          355          360          365
Arg Gly Gly Lys Tyr Ala Val Gly Ser Ala Cys Ile Gly Gly Gly Gln
          370          375          380
Gly Ile Ala Val Ile Ile Gln Ser Thr Ala
385          390

```

```

<210> 77
<211> 1642
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..68

```

```

<220>
<221> CDS
<222> 69..875

```

```

<220>
<221> 3'UTR
<222> 876..1642

```

```

<220>
<221> polyA_signal
<222> 1599..1604

```

```

<220>
<221> polyA_site
<222> 1627..1642

```

```

<400> 77
attttatagc ggccgcgggc ggccgcggca gcggttgag gttgtaggac cggcgaggaa 60
taggaatc atg gcg gct gcg ctg ttc gtg ctg ctg gga ttc gcg ctg ctg 110
      Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu
      -20          -15          -10
ggc acc cac gga gcc tcc ggg gct gcc ggc aca gtc ttc act acc gta 158
Gly Thr His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val
      -5          1          5          10
gaa gac ctt ggc tcc aag ata ctc ctc acc tgc tcc ttg aat gac agc 206
Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser
      15          20          25
gcc aca gag gtc aca ggg cac cgc tgg ctg aag ggg ggc gtg gtg ctg 254
Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu
      30          35          40
aag gag gac gcg ctg ccc ggc cag aaa acg gag ttc aag gtg gac tcc 302
Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser
      45          50          55
gac gac cag tgg gga gag tac tcc tgc gtc ttc ctc ccc gag ccc atg 350
Asp Asp Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met
      60          65          70
ggc acg gcc aac atc cag ctc cac ggg cct ccc aga gtg aag gcc gtg 398
Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val
      75          80          85          90
aag tcg tca gaa cac atc aac gag ggg gag acg gcc atg ctg gtc tgc 446
Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys
      95          100          105

```


Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser
80 85 90
Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser
95 100 105
Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp
110 115 120
Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val
125 130 135
Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu Asn Met
140 145 150 155
Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly
160 165 170
Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala
175 180 185
Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr
190 195 200
Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp
205 210 215
Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln
220 225 230 235
Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
240 245

<210> 79
<211> 1466
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..343

<220>
<221> CDS
<222> 344..1144

<220>
<221> 3'UTR
<222> 1145..1466

<400> 79
attgtgactt tgggccaggc tgggggaaat gaccggggag ggtcccatgc ggctacataa 60
aattggcagc cttagaacta gtgggaaggc ggggtgcgca agtcgagggg cggagagagg 120
gggcccggagg agctgctttc tgaatccaag ttcgtgggct ctctcagaag tcttcaggac 180
ggagcagagg tggccggcgg gcccggtga ctgcgcctyt gctttctttc cataaccttt 240
tctttcggac tcgaatcacg gctgctgcga aggggtctagt tccggacact aggggtgcccg 300
aacgcgctga tgccccgagt gctcgcaggg cttcccgcta acc atg ctg ccg ccg 355
Met Leu Pro Pro
ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc ctg cta ctg ctg 403
Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu Leu Leu Leu Leu
-25 -20 -15 -10
gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca tcc cca ggc cca 451
Val Val Leu Thr Pro Pro Thr Gly Ala Arg Pro Ser Pro Gly Pro
-5 1 5
gat tac ctg cgg cgc ggc tgg atg cgg ctg cta gcg gag ggc gag ggc 499
Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala Glu Gly Glu Gly
10 15 20
tgc gct ccc tgc cgg cca gaa gag tgc gcc gcg ccg cgg ggc tgc ctg 547
Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro Arg Gly Cys Leu
25 30 35
gcg ggc agg gtg cgc gac gcg tgc ggc tgc tgc tgg gaa tgc gcc aac 595
Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp Glu Cys Ala Asn
40 45 50 55

55 60 65
 His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr
 70 75 80
 Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys
 85 90 95
 Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln
 100 105 110
 Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu
 115 120 125 130
 Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser
 135 140 145
 His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly
 150 155 160
 Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
 165 170 175
 Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
 180 185 190
 Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
 195 200 205 210
 Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro
 215 220 225
 Met Pro Trp Val Lys Trp Arg Pro Leu Leu Ala
 230 235

<210> 81
 <211> 1406
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..26

<220>
 <221> CDS
 <222> 27..689

<220>
 <221> 3'UTR
 <222> 690..1406

<220>
 <221> polyA_signal
 <222> 1302..1307

<220>
 <221> polyA_site
 <222> 1325..1406

<400> 81
 cccggaagtg cgcaggcgct ggcaag atg gcg gga ggg gtg cgc ccg ctg cgg 53
 Met Ala Gly Gly Val Arg Pro Leu Arg
 -30 -25
 ggc ctc cgc gcc ttg tgt cgc gtg ctg ctc ttc ctt tcg cag ttc tgc 101
 Gly Leu Arg Ala Leu Cys Arg Val Leu Leu Phe Leu Ser Gln Phe Cys
 -20 -15 -10
 att ctg tcg ggc ggt gaa agt act gaa atc cca cct tat gtg atg aag 149
 Ile Leu Ser Gly Gly Glu Ser Thr Glu Ile Pro Pro Tyr Val Met Lys
 -5 1 5 10
 tgt ccg agc aat ggt ttg tgt agc agg ctt cct gca gac tgt ata gac 197
 Cys Pro Ser Asn Gly Leu Cys Ser Arg Leu Pro Ala Asp Cys Ile Asp
 15 20 25
 tgc aca aca aat ttc tcc tgt acc tat ggg aag cct gtc act ttt gac 245

Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Ala Val Lys Pro Ser Val
 35 40 45
 Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Asn Phe Ile Ile Asn
 50 55 60
 Met Thr Cys Arg Phe Cys Trp Gln Leu Pro Glu Thr Asp Tyr Glu Cys
 65 70 75 80
 Thr Asn Ser Thr Ser Cys Met Thr Val Ser Cys Pro Arg Gln Arg Tyr
 85 90 95
 Pro Ala Asn Cys Thr Val Arg Asp His Val His Cys Leu Gly Asn Arg
 100 105 110
 Thr Phe Pro Lys Met Leu Tyr Cys Asn Trp Thr Gly Gly Tyr Lys Trp
 115 120 125
 Ser Thr Ala Leu Ala Leu Ser Ile Thr Leu Gly Gly Phe Gly Ala Asp
 130 135 140
 Arg Phe Tyr Leu Gly Gln Trp Arg Glu Gly Leu Gly Lys Leu Phe Ser
 145 150 155 160
 Phe Gly Gly Leu Gly Ile Trp Thr Leu Ile Asp Val Leu Leu Ile Gly
 165 170 175
 Val Gly Tyr Val Gly Pro Ala Asp Gly Ser Leu Tyr Ile
 180 185

<210> 83
 <211> 1754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..117

<220>
 <221> CDS
 <222> 118..510

<220>
 <221> 3'UTR
 <222> 511..1754

<220>
 <221> polyA_signal
 <222> 1718..1723

<220>
 <221> polyA_site
 <222> 1739..1754

<400> 83
 tccccggccg ccgcggttgc gtcgcccgcg ctgcgactga agcccggggc ctcgcgcgcc 60
 gcggttcgcc ccgcagctc gccccctgcc caccggggcg gccgtagggc ggtaacg 117
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe

<210> 85
 <211> 1754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..117

<220>
 <221> CDS
 <222> 118..510

<220>
 <221> 3'UTR
 <222> 511..1754

<220>
 <221> polyA_signal
 <222> 1718..1723

<220>
 <221> polyA_site
 <222> 1739..1754

<400> 85
 tccccggccg ccgcggttgc gctcgcgcgcg ctgcactga agccccgggcc ctgcgcgcgc 60
 gcggttcgcc ccgcagcctc gccccctgcc caccgggcg gccgtagggc gggtcacg 117
 atg ctg ccg ccc tta ccc tcc cgc ctg ggg ctg ctg ctg ctg ctg 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct cgg ggc gcc cgg ctg ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
 75 80 85
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
 90 95 100 105
 ggc ccc agc tgaccgcccc agccccgcgt gattgcacct gtctgcattc 550
 Gly Pro Ser
 acagacattc gggagacggc ctctgtgttc gccatcactg cggcgggcgc cagccacggc 610
 gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
 cgggccccctc cccggcccc cggcctgccc ggcaccccc gacccccctg ccccgcgggc 730
 tccccggaag gcagcgccgc ctgggagtgg ggaggctgcg gcgacgacgt ggacttcggg 790
 gacgagaagt cgaggctctt tatggacgcg cggcacaagc ggggacgcgg agacatccgc 850
 gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg ccgtgcggag ccacacgcgc 910
 accgagtgc aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970
 ctgcctccat ttgcgaggt gggcgcgcg ctgctggagc gcttycacgg cgctcacgc 1030
 gtcattgggca ccaacgacgg caaggccctg ctgccccgcg tccgcacgct caagccgccc 1090

```

ggccgagcgg acctcctcta cgcgcgcgat tcgcccgcact tctgcgcccc caaccgacgc 1150
accggctccc ccggcacgcg cggtcgcgcc tgcaatagca gcgccccgga cctcagcggc 1210
tgcgacctgc tgtgctgcgg ccgcgggcac cgccaggaga gcgtgcagct cgaagagaac 1270
tgccgtgccc gcttccactg gtgctgcgta gtacagtgcc accgctgcgg tgtgcgcaag 1330
gagctcagcc tctgcctgtg acccgccgcc cgcccgctag actgacttcg cgcagcgggtg 1390
gctcgcacct gtgggacctc agggcaccgg caccggggcg ctctcgccgc tcgagcccag 1450
cctctccctg ccaaagccca actcccaggg ctctggaaat ggtgaggcga ggggcttgag 1510
aggaacgccc acccacgaag gcccagggcg ccagacggcc ccgaaaaggc gctcggggag 1570
cgtttaaagg aactgtaca ggcctccct ccccttggcc tctaggagga aacagtttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
cacaggatgg tgggtgaggt tagtatcaat aaagatatatt aaaccaccaa aaaaaaaaaa 1750
aaaa

```

```

<210> 86
<211> 131
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..24

```

```

<400> 86
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
                                -20                    -15                -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
                                -5                      1                5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
                                10                      15                20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
25                               30                      35                40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
                                45                      50                55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
                                60                      65                70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
                                75                      80                85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
90                               95                      100
Gly Pro Ser
105

```

```

<210> 87
<211> 1431
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..151

```

```

<220>
<221> CDS
<222> 152..655

```

```

<220>
<221> 3'UTR
<222> 656..1431

```

```

<220>
<221> polyA_signal
<222> 1399..1404

```

<220>
 <221> polyA_site
 <222> 1416..1431

<400> 87

```

aattttttct cacaaggact ggggtgaagag ttctgcagcc ttacagagac tggaaaagaa 60
gcccaaacca agggccccag agaggtcccc caggccccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
                                Met Leu Phe Arg Leu Ser Glu
                                1           5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
                                10           15           20
gag ggg cac cat ctc aag tgc aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
                                25           30           35
cca cct tgc ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
                                40           45           50           55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
                                60           65           70
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
                                75           80           85
gaa gag gag gat gat gaa gaa gag gaa gaa gag gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
                                90           95           100
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
                                105           110           115
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
                                120           125           130           135
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
                                140           145           150
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
                                155           160           165
aca taggcacca gctgcatct cccaggagga agtggagggg acatcgctgt 705
Thr
tccccagaaa ccactctat cctcaccctg ttttgtgctc ttcccctcgc ctgctagggc 765
tgcggtttct gacttctaga agactaaggc tgggtctgtgt ttgcttggtt gccaccttt 825
ggctgatacc cagagaacct gggcacttgc tgcctgatgc ccaccctgc cagtcattcc 885
tccattcacc cagcgggagg tgggatgtga gacagccac attggaaaat ccagaaaacc 945
gggaacaggg atttgccctt cacaattcta ctccccagat cctctccctt ggacacagga 1005
gacccacagg gcaggacct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065
cttagatcct tttctacca ctttctatg gaggattcca agtcaccact tctctaccg 1125
gcttctacca ggttccagga ctaaggcgtt tttctccata gcctcaacat tttgggaatc 1185
ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245
tgttgcggtt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305
acagcggggg gcgccagggt ttcttgtcc cccagctgct ctgccccttt ccccttcttc 1365
cctgactcca ggctgaacc cctcccgctg tgtaataaat ctttgtaaag aaaaaaaaaa 1425
aaaaaa 1431

```

<210> 88
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 88

Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser

```

1             5             10             15
Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
      20             25             30
Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg
      35             40             45
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
      50             55             60
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
65             70             75             80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
      85             90             95
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
      100            105            110
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
      115            120            125
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
      130            135            140
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
145            150            155            160
Pro Ser Pro Ser Glu Pro Gly Thr
      165

```

```

<210> 89
<211> 1431
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..151

```

```

<220>
<221> CDS
<222> 152..655

```

```

<220>
<221> 3'UTR
<222> 656..1431

```

```

<220>
<221> polyA_signal
<222> 1399..1404

```

```

<220>
<221> polyA_site
<222> 1416..1431

```

```

<400> 89
aatTTTTtct cacaaggact gggTgaagag ttctgcagcc ttacagagac tggaaaagaa 60
gcccaaacca aggcccccag agaggtcccc caggccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
Met Leu Phe Arg Leu Ser Glu
      1             5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
      10             15             20
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
      25             30             35
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
      40             45             50             55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364

```


<400> 91																		
ctcctcagct	tcaggcacca	ccactgacct	gggacagtga	atcgaca	atg	ccg	tct											56
					Met	Pro	Ser											
tct	gtc	tcg	tgg	ggc	atc	ctc	ctg	ctg	gca	ggc	ctg	tgc	tgc	ctg	gtc			104
Ser	Val	Ser	Trp	Gly	Ile	Leu	Leu	Leu	Ala	Gly	Leu	Cys	Cys	Leu	Val			
-20					-15					-10								
cct	gtc	tcc	ctg	gct	gat	ccc	cag	gga	gat	gct	gcc	cag	aag	aca				152
Pro	Val	Ser	Leu	Ala	Glu	Asp	Pro	Gln	Gly	Asp	Ala	Ala	Gln	Lys	Thr			
				1				5					10					
gat	aca	tcc	cac	cat	gat	cag	gat	cac	cca	acc	ttc	aac	aag	atc	acc			200
Asp	Thr	Ser	His	His	Asp	Gln	Asp	His	Pro	Thr	Phe	Asn	Lys	Ile	Thr			
				15				20					25					
ccc	aac	ctg	gct	gag	ttc	gcc	ttc	agc	cta	tac	cgc	cag	ctg	gca	cac			248
Pro	Asn	Leu	Ala	Glu	Phe	Ala	Phe	Ser	Leu	Tyr	Arg	Gln	Leu	Ala	His			
						35						40						
cag	tcc	aac	agc	acc	aat	atc	ttc	ttc	tcc	cca	gtg	agc	atc	gct	aca			296
Gln	Ser	Asn	Ser	Thr	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Ile	Ala	Thr			
						50						55						
gcc	ttt	gca	atg	ctc	tcc	ctg	ggg	acc	aag	gct	gac	act	cac	gat	gaa			344
Ala	Phe	Ala	Met	Leu	Ser	Leu	Gly	Thr	Lys	Ala	Asp	Thr	His	Asp	Glu			
						65				70					75			
atc	ctg	gag	agc	ctg	aat	ttc	aac	ctc	acg	gag	att	ccg	gag	gct	cag			392
Ile	Leu	Glu	Ser	Leu	Asn	Phe	Asn	Leu	Thr	Glu	Ile	Pro	Glu	Ala	Gln			
						80				85					90			
atc	cat	gaa	ggc	ttc	cag	gaa	ctc	cgt	acc	ctc	aac	cag	cca	gac				440
Ile	His	Glu	Gly	Phe	Gln	Glu	Leu	Leu	Arg	Thr	Leu	Asn	Gln	Pro	Asp			
							100					105						
agc	cag	ctc	cag	ctg	acc	acc	ggc	aat	ggc	ctg	ttc	ctc	agc	gag	ggc			488
Ser	Gln	Leu	Gln	Leu	Thr	Thr	Gly	Asn	Gly	Leu	Phe	Leu	Ser	Glu	Gly			
							110					120						
ctg	aag	cta	gtg	gat	aag	ttt	ttg	gag	gat	gtt	aaa	aag	ttg	tac	cac			536
Leu	Lys	Leu	Val	Asp	Lys	Phe	Leu	Glu	Asp	Val	Lys	Lys	Leu	Tyr	His			
						125				135					140			
tca	gaa	gcc	ttc	act	gtc	aac	ttc	ggg	gac	acc	gaa	gag	gcc	aag	aaa			584
Ser	Glu	Ala	Phe	Thr	Val	Asn	Phe	Gly	Asp	Thr	Glu	Glu	Ala	Lys	Lys			
						145				150					155			

<221> 3'UTR
<222> 734..1115

<220>
<221> polyA_signal
<222> 1072..1077

<220>
<221> polyA_site
<222> 1101..1115

<400> 93
ctcttttgctc taacagacag cagcgacttt aggctggata atagtcaaat tcttacctcg 60
ctcttttact gctagtaaga tcagattgcg tttctttcag ttactcttca atcgccagtt 120
tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
ggaaaaacaa aataacctca actccgtttt gaaaaaaaca ttccaagaac ttcatcaga 240
gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295
Met His Phe Gly Leu Leu
-15
tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
-10 -5 1
gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391
Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu
5 10 15 20
aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439
Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
25 30 35
aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487
Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys
40 45 50
gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535
Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu
55 60 65
agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583
Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg
70 75 80
att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631
Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu
85 90 95 100
gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679
Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr
105 110 115
aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727
Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp
120 125 130
gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggg 783
Ala Ile
ccgaatgggt tccagggtgga taattatgga acccagctca atgctgtgaa taactccctg 843
actccgcaat caaccaaggt tcccagcctt tttgttacaa aagaaggaaac aaatgatggg 903
tggaagaatg cggctcatat ttaccaagtc tttctgaacg cctttctgcat tcatgcatcc 963
atgttctttc taggattgga tagcatttca tgcctatggt aatattttgtg cttttggcat 1023
ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083
atattttacat gcataggaaa aaaaaaaaaa aa 1115

<210> 94
<211> 152
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..19

<400> 94
 Met His Phe Gly Leu Leu Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro
 -15 -10 -5
 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
 1 5 10
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
 15 20 25
 Ala Asp Asp Ser Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
 30 35 40 45
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
 50 55 60
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
 65 70 75
 Arg Asp Asn Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys
 80 85 90
 Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr
 95 100 105
 Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys His Val Asn Val Ser
 110 115 120 125
 Ser Met Val Asp Ala Trp Ala Ile
 130

<210> 95
 <211> 1307
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..252

<220>
 <221> CDS
 <222> 253..744

<220>
 <221> 3'UTR
 <222> 745..1307

<220>
 <221> polyA_signal
 <222> 1269..1274

<220>
 <221> polyA_site
 <222> 1292..1307

<400> 95
 ctctttgctc taacagacag cagcgacttt aggctggata atagtcaa atcttacctcg 60
 ctctttcact gctagtaaga tcagattgcg tttctttcag ttactcttca atcgccagtt 120
 tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
 ggaaaaacag aataacctca actccgtttt gaaaaaaaca ttccaagaac ttctatcaga 240
 gattttactt ag atg att tac aca atg aag aaa gta cat gca ctt tgg gct 291
 Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala
 -25 -20 -15
 tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat 339
 Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp
 -10 -5 1
 tct gag gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca 387
 Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro
 5 10 15
 cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat ggc 435

Asn Gln Gln Phe
135

<210> 97
<211> 1855
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..117

<220>
<221> CDS
<222> 118..504

<220>
<221> 3'UTR
<222> 505..1855

<220>
<221> polyA_signal
<222> 1819..1824

<220>
<221> polyA_site
<222> 1840..1855

<400> 97
tccccggcgc cgcgcgttgc gtcgcgcgcg ctgcactga agccccgggcc ctgcgcgcgc 60
gcggttcgcc cgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117
atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
-20 -15 -10
ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20 25
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
30 35 40
ctg gct ccg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
75 80 85
tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
90 95 100 105
gcc tgagccccac ttccccctca catgtgtctg ggcaccctgc aaggaccctg 554
Ala
cctcccaggc ccctggggca gccctccgcg cgcaggtttc aggtcccagg cccagctga 614
ccgccccagc ccgcgctgat tgcacctgtc tgcattcaca gacattcggg agacggcctt 674
cgtgttcgcc atcactgcgg ccggcgccag ccacgcgcgc acgcaggcct gttctatggg 734
cgagctgctg cagtgcggct gccaggcgcc ccgcggggcg gccctcccc ggccctccgg 794
cctgcccggc acccccggac cccctggccc cgcgggctcc ccggaaggca gcgcccgcctg 854
ggagtgggga ggctgcggcg acgacgtgga cttcggggac gagaagtcga ggctctttat 914

```

ggacgcgcgcg cacaagcggg gacgcggaga catccgcgcg ttggtgcaac tgcacaacaa 974
cgaggcgggc aggctggccg tgcggagcca cagcgcgacc gaggcgaat gccacgggct 1034
gtcgggatca tgcgcgctgc gcacctgctg gcagaagctg cctccatttc gcgaggtggg 1094
cgcgcgcgctg ctggagcgct tccacggcgc ctacgcgctc atgggcacca acgacggcaa 1154
ggccctgctg cccgcgctcc gcacgctcaa gccgcggggc cgagcggacc tcctctacgc 1214
cgccgattcg cccgacttct gcgcccccaa ccgacgcacc ggctcccccg gcacgcgcgcg 1274
tcgcgcctgc aatagcagcg ccccggaact cagcggctgc gacctgctgt gctgcggccg 1334
cgggcaccgc caggagagcg tgcagctcga agagaactgc ctgtgccgct tccactggtg 1394
ctgcgtagta cagtgccacc gctgccgtgt gcgcaaggag ctgagcctct gcctgtgacc 1454
cgccgcccgg ccgctagact gacttcgcgc agcgggtggc cgcacctgtg ggacctcagg 1514
gcaccggcac cgggcgcctc tcgcgcctcg agcccagcct ctccctgcca aagcccaact 1574
cccagggtc tggaaatggt gaggcgaggg gcttgagagg aacgcccacc cacgaaggcc 1634
cagggcgcca gacggccccg aaaaggcgct cggggagcgt ttaaaggaca ctgtacaggc 1694
cctccctccc cttggcctct aggaggaaac agtttttag actggaaaaa agccagtcta 1754
aaggcctctg gatactgggc tccccagaac tgctggccac aggatggtgg gtgaggttag 1814
tatcaataaa gatatttaaa ccacaaaaaa aaaaaaaaaa a 1855

```

```

<210> 98
<211> 129
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..24

```

```

<400> 98
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
-20 -15 -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
25 30 35 40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
75 80 85
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
90 95 100
Ala
105

```

```

<210> 99
<211> 667
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..94

<220>
<221> CDS
<222> 95..613

```

```

<220>
<221> 3'UTR
<222> 614..667

```

[illegible][illegible][illegible][illegible][illegible]

65		70		75		80									
His	Gly	Tyr	Ala	Phe	Ala	Ile	Thr	Asn	Asn	Gly	Tyr	Ile	Leu	Thr	His
			85					90					95		
Pro	Glu	Leu	Arg	Leu	Leu	Tyr	Glu	Glu	Gly	Lys	Lys	Arg	Arg	Lys	Pro
		100						105					110		
Asn	Tyr	Ser	Ser	Val	Asp	Leu	Ser	Glu	Val	Glu	Trp	Glu	Asp	Arg	Asp
		115					120					125			
Asp	Val	Leu	Arg	Asn	Ala	Met	Val	Asn	Arg	Lys	Thr	Gly	Lys	Phe	Ser
	130					135					140				
Met	Glu	Val	Lys	Lys	Thr	Val	Asp	Lys	Gly	Val	His	Phe	Ser	Gln	Thr
145					150					155				160	
Phe	Leu	Leu	Leu	Asn	Leu	Lys	Gln	Thr	Thr	Val	Lys	Asn			
			165					170							

<210> 101
 <211> 1062
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..153

<220>
 <221> CDS
 <222> 154..639

<220>
 <221> 3'UTR
 <222> 640..1062

<220>
 <221> polyA_signal
 <222> 1023..1028

<220>
 <221> polyA_site
 <222> 1047..1062

<400> 101	
attggtgtat ggctttgcag caataactga tggctgtttc ccctcctgct ttatctttca	60
gttaatgacc agccacggcg tccctgctgt gagctctggc cgctgccttc cagggctccc	120
gagccacacg ctgggggtgc tggctgaggg aac atg gct tgt tgg cct cag ctg	174
	Met Ala Cys Trp Pro Gln Leu
	1 5
agg ttg ctg ctg tgg aag aac ctc act ttc aga aga aga caa aca tgt	222
Arg Leu Leu Leu Trp Lys Asn Leu Thr Phe Arg Arg Arg Gln Thr Cys	
	10 15 20
cag ctg ctg ctg gaa gtg gcc tgg cct cta ttt atc ttc ctg atc ctg	270
Gln Leu Leu Leu Glu Val Ala Trp Pro Leu Phe Ile Phe Leu Ile Leu	
	25 30 35
atc tct gtt cgg ctg agc tac cca ccc tat gaa caa cat gaa tgc cat	318
Ile Ser Val Arg Leu Ser Tyr Pro Pro Tyr Glu Gln His Glu Cys His	
	40 45 50 55
ttt cca aat aaa gcc atg ccc tct gca gga aca ctt cct tgg gtt cag	366
Phe Pro Asn Lys Ala Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln	
	60 65 70
ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct	414
Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro	
	75 80 85
ggg gag gct ccc gga gtt gtt gga aac ttt aac aaa tcc att gtg gct	462
Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala	
	90 95 100

```

cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac 510
Arg Leu Phe Ser Asp Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp
105 110 115
acc agc atg aag gac atg cgc aaa gtt ctg aga aca tta cag cag atc 558
Thr Ser Met Lys Asp Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile
120 125 130 135
aag aaa tcc agc tca aga ggg gac aaa cgc cat ttc ctc aac tgg cag 606
Lys Lys Ser Ser Arg Arg Gly Asp Lys Arg His Phe Leu Asn Trp Gln
140 145 150
aag gga ctg aag cct ctc cct caa gcc ctt tta taggggtcct cattgtcagg 659
Lys Gly Leu Lys Pro Leu Pro Gln Ala Leu Leu
155 160
cctctaagcc caagccaagc catcgcatcc cctgtgactt gcacatatat gccagatgg 719
cctgaagtaa ctgaagaatc acaaaagaag tgaaaaggcc ctgcctcgcc ttaactgatg 779
acgttcacc attgtgattt gttcctgccc caccttaact gattgattaa ccctgtgaat 839
ttccttctcc tggctcagaa gctccccac tgagcacctt gtgacccct gccctgccc 899
accagagaac aacccccctt gactgtaatt ttccattacc ttccaaatc ctataaaacg 959
gccccacccc tatctccctt tgetgactct cttttcggac tcagcccacc tgcagccagg 1019
tgaaaaaaac agctttattg ctcacacaaa aaaaaaaaaa aaa 1062

```

<210> 102
 <211> 162
 <212> PRT
 <213> Homo sapiens

```

<400> 102
Met Ala Cys Trp Pro Gln Leu Arg Leu Leu Leu Trp Lys Asn Leu Thr
1 5 10 15
Phe Arg Arg Arg Gln Thr Cys Gln Leu Leu Leu Glu Val Ala Trp Pro
20 25 30
Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro
35 40 45
Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala
50 55 60
Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro
65 70 75 80
Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn
85 90 95
Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu
100 105 110
Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val
115 120 125
Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Arg Gly Asp Lys
130 135 140
Arg His Phe Leu Asn Trp Gln Lys Gly Leu Lys Pro Leu Pro Gln Ala
145 150 155 160
Leu Leu

```

<210> 103
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..149

<220>
 <221> CDS
 <222> 150..392

<220>
 <221> 3'UTR

<222> 393..933

<220>

<221> polyA_site

<222> 63..933

<400> 103

```
aaaccctcag ggacctggtg tagacgcaga atctgtttca cacaacaact gctatttgaa 60
ggaaaaaaaa aaaaagaagc aaatgatacc aagacaagct cataacagag atccaatcag 120
cagatgtgta cggatgaaaa tacagtgtg atg agt cag aaa ccg gcc aag gag 173
                               Met Ser Gln Lys Pro Ala Lys Glu
                               1         5
ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
   10         15         20
cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
   25         30         35         40
gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317
Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
           45         50         55
gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
           60         65         70
aag atc agg cca acc cca aag aag aag tgaccaagga ggagtttaaa 412
Lys Ile Arg Pro Thr Pro Lys Lys Lys
           75         80
ytgaatgaac aacctcggct cctggactca ttgcttcaca acccatctac ccctggatga 472
agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532
gctcatgggc cccatggcat gggggcctca gggcagcctg cctggagtac tttgaagatg 592
tcatccatt gtcttctgac ctctataatt gccactgaga gatctgctgt cagtctgctt 652
atccttcac ggactcaagt ttcttcaatc tgaagataca tgtctttctc caaggacatg 712
tggaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772
gcgtgggtgg gggcgccctgt ggtcccagct actcgggagg ctgaggcagg agaatggcgt 832
gaacctggga ggcggagctt gcagtgcgc gagatcgcac cactgcactc cagcctgggc 892
gacagagcga gactctgtct caaacaaaaa aaaaaaaaaa a 933
```

<210> 104

<211> 81

<212> PRT

<213> Homo sapiens

<400> 104

```
Met Ser Gln Lys Pro Ala Lys Glu Gly Pro Arg Leu Ser Lys Asn Gln
1         5         10         15
Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
   20         25         30
Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys
   35         40         45
Ser Gly Cys Phe Tyr Gln Lys Lys Glu Glu Asp Trp Ile Cys Cys Ala
   50         55         60
Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys
   65         70         75         80
Lys
```

<210> 105

<211> 1187

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..34

<220>
 <221> CDS
 <222> 35..1069

<220>
 <221> 3'UTR
 <222> 1070..1187

<220>
 <221> polyA_signal
 <222> 1146..1151

<220>
 <221> polyA_site
 <222> 1172..1187

<400> 105
 accactttgg tagtgccagt gtgactcatc caca atg att tct cca gtg ctc atc 55
 Met Ile Ser Pro Val Leu Ile
 -15
 ttg ttc tcg agt ttt ctc tgc cat gtt gct att gca gga cgg acc tgt 103
 Leu Phe Ser Ser Phe Leu Cys His Val Ala Ile Ala Gly Arg Thr Cys
 -10 -5 1 5
 ccc aag cca gat gat tta cca ttt tcc aca gtg gtc ccg tta aaa aca 151
 Pro Lys Pro Asp Asp Leu Pro Phe Ser Thr Val Val Pro Leu Lys Thr
 10 15 20
 ttc tat gag cca gga gaa gag att acg tat tcc tgc aag ccg ggc tat 199
 Phe Tyr Glu Pro Gly Glu Glu Ile Thr Tyr Ser Cys Lys Pro Gly Tyr
 25 30 35
 gtg tcc cga gga ggg atg aga aag ttt atc tgc cct ctc aca gga ctg 247
 Val Ser Arg Gly Gly Met Arg Lys Phe Ile Cys Pro Leu Thr Gly Leu
 40 45 50
 tgg ctc atc aac act ctg aaa tgt aca ccc aga gta tgt cct ttt gct 295
 Trp Leu Ile Asn Thr Leu Lys Cys Thr Pro Arg Val Cys Pro Phe Ala
 55 60 65
 gga atc tta gaa aat gga gcc gta cgc tat acg act ttt gaa tat ccc 343
 Gly Ile Leu Glu Asn Gly Ala Val Arg Tyr Thr Thr Phe Glu Tyr Pro
 70 75 80 85
 aac acg atc agt ttt tct tgt aac act ggg ttt tat ctg aat ggc gct 391
 Asn Thr Ile Ser Phe Ser Cys Asn Thr Gly Phe Tyr Leu Asn Gly Ala
 90 95 100
 gat tct gcc aag tgc act gag gaa gga aaa tgg agc ccg gag ctt cct 439
 Asp Ser Ala Lys Cys Thr Glu Glu Gly Lys Trp Ser Pro Glu Leu Pro
 105 110 115
 gtc tgt gct ccc atc atc tgc cct cca cca tcc ata cct acg ttt gca 487
 Val Cys Ala Pro Ile Ile Cys Pro Pro Pro Ser Ile Pro Thr Phe Ala
 120 125 130
 aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg 535
 Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg
 135 140 145
 gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat 583
 Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn
 150 155 160 165
 gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa 631
 Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu
 170 175 180
 tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt 679
 Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe
 185 190 195
 gtg aac tat cct gca aaa cca aca ctt tat tac aag gat aaa gcc aca 727
 Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr
 200 205 210

Arg Thr Leu Lys Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser
 430 435 440
 ttc cag agg agg aat atg atc gag cct cga gag aga gcc aag ttc aaa 1395
 Phe Gln Arg Arg Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys
 445 450 455 460
 cgc aag tac aag gtg aag ctg gtg gag aag cgg gcg ttc cgt gag atc 1443
 Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile
 465 470 475
 cag ttg tagctgccat cagatgccgg agactcgccc ttcaataaaa aatctcttct 1499
 Gln Leu
 agtcaaaaa aaaaaaaaaa a 1520

<210> 108
 <211> 478
 <212> PRT
 <213> Homo sapiens

<400> 108
 Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg Ser Ser Lys Ser
 1 5 10 15
 Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr Ser Val Asp Pro
 20 25 30
 Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp
 35 40 45
 Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu
 50 55 60
 Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu
 65 70 75 80
 Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys
 85 90 95
 Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu
 100 105 110
 Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val
 115 120 125
 Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys
 130 135 140
 Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu
 145 150 155 160
 Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser
 165 170 175
 Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe
 180 185 190
 Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly
 195 200 205
 Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg
 210 215 220
 Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val
 225 230 235 240
 Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr
 245 250 255
 Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala
 260 265 270
 Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr Glu Gln Ala Ala
 275 280 285
 Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu
 290 295 300
 Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly
 305 310 315 320
 Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala Thr Thr Glu Lys
 325 330 335
 Lys Thr Glu Gln Arg Arg Arg Glu Lys Ala Val His Arg Leu Arg
 340 345 350
 Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg His Gln Glu Leu

taaaaaaatgt tctcttggtt caaaaaaaaa aaaaaaa

1789

<210> 110

<211> 386

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..15

<400> 110

Met Cys Leu Leu Leu Ser Cys Pro Cys His Pro Ser Ala His Gly Gln
-15 -10 -5 1
Ser Met Trp Ile Glu Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro
5 10 15
Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile
20 25 30
Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys
35 40 45
Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile
50 55 60 65
Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met
70 75 80
Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val
85 90 95
Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu
100 105 110
Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu
115 120 125
Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu
130 135 140 145
Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg
150 155 160
Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met
165 170 175
Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn
180 185 190
Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu
195 200 205
Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile
210 215 220 225
Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys
230 235 240
Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala
245 250 255
Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp
260 265 270
Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu
275 280 285
Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu
290 295 300 305
Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser
310 315 320
Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys
325 330 335
Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala
340 345 350
Ser Lys Ser Ala Glu Glu Gly Lys Gln Ile Pro Asp Ser Leu Ser Thr
355 360 365
Asp Leu
370

<210> 111
 <211> 1408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..102

<220>
 <221> CDS
 <222> 103..1263

<220>
 <221> 3'UTR
 <222> 1264..1408

<220>
 <221> polyA_signal
 <222> 1341..1346

<220>
 <221> polyA_site
 <222> 1365..1408

<400> 111
 cttcttgact ctctgttcac agaactcagg ctgcctccag ccagcctttg cccgctagac 60
 tcactggccc tgatcacttg aaggtgcagc aagtcactga ga atg agc act ttc 114
 Met Ser Thr Phe
 1
 ttc tcg gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt 162
 Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys
 5 10 15 20
 ggg aca gta ttt tgc aaa tac aag aag agc tca ggg cag ctg tgg agc 210
 Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly Gln Leu Trp Ser
 25 30 35
 tgg atg gtc tgc ctg gca ggc ctc tgt gca gtc tgc ctg ctc atc ctg 258
 Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Leu Ile Leu
 40 45 50
 tcc cct ttt tgg ggc ttg atc ctc ttc tcg gtg tca tgc ttc ctc atg 306
 Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met
 55 60 65
 tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca 354
 Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala
 70 75 80
 gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag 402
 Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys
 85 90 95 100
 tat ctg gat gag ctg ggc ttc acg gta ttt gcc gga gtt ttg aat gaa 450
 Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly Val Leu Asn Glu
 105 110 115
 aat ggc cca gga gct gag gaa ttg cga aga acc tgc tct ccg cgc ctc 498
 Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys Ser Pro Arg Leu
 120 125 130
 tcg gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct 546
 Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala
 135 140 145
 tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg 594
 Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val
 150 155 160
 atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt 642
 Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu
 165 170 175 180

Val	Leu	Asn	Glu	Asn	Gly	Pro	Gly	Ala	Glu	Glu	Leu	Arg	Arg	Thr	Cys	
		115					120					125				
Ser	Pro	Arg	Leu	Ser	Val	Leu	Gln	Met	Asp	Ile	Thr	Lys	Pro	Val	Gln	
		130				135						140				
Ile	Lys	Asp	Ala	Tyr	Ser	Lys	Val	Ala	Ala	Met	Leu	Gln	Asp	Arg	Gly	
145					150					155					160	
Leu	Trp	Ala	Val	Ile	Asn	Asn	Ala	Gly	Val	Leu	Gly	Phe	Pro	Thr	Asp	
				165					170						175	
Gly	Glu	Leu	Leu	Leu	Met	Thr	Asp	Tyr	Lys	Gln	Cys	Met	Ala	Val	Asn	
			180					185						190		
Phe	Phe	Gly	Thr	Val	Glu	Val	Thr	Lys	Thr	Phe	Leu	Pro	Leu	Leu	Arg	
		195					200					205				
Lys	Ser	Lys	Gly	Arg	Leu	Val	Asn	Val	Ser	Ser	Met	Gly	Gly	Gly	Ala	
		210				215					220					
Pro	Val	Glu	Arg	Leu	Ala	Ser	Tyr	Gly	Ser	Ser	Lys	Ala	Ala	Val	Thr	
225					230					235					240	
Met	Phe	Ser	Ser	Val	Met	Arg	Leu	Glu	Leu	Ser	Lys	Trp	Gly	Ile	Lys	
				245					250						255	
Val	Ala	Ser	Ile	Gln	Pro	Gly	Gly	Phe	Leu	Thr	Asn	Ile	Ala	Gly	Thr	
			260					265					270			
Ser	Asp	Lys	Trp	Glu	Lys	Leu	Glu	Lys	Asp	Ile	Leu	Asp	His	Leu	Pro	
		275					280					285				
Ala	Glu	Val	Gln	Glu	Asp	Tyr	Cys	Gln	Asp	Tyr	Ile	Leu	Ala	Gln	Arg	
		290				295					300					
Asn	Phe	Leu	Leu	Leu	Ile	Asn	Ser	Leu	Ala	Ser	Lys	Asp	Phe	Ser	Pro	
305					310					315					320	
Val	Leu	Arg	Asp	Ile	Gln	His	Ala	Ile	Leu	Ala	Lys	Ser	Pro	Phe	Ala	
				325					330						335	
Tyr	Tyr	Thr	Pro	Gly	Lys	Gly	Ala	Tyr	Leu	Trp	Ile	Cys	Leu	Ala	His	
			340					345						350		
Tyr	Leu	Pro	Ile	Gly	Ile	Tyr	Asp	Tyr	Phe	Ala	Lys	Arg	His	Phe	Gly	
		355					360					365				
Gln	Asp	Lys	Pro	Met	Pro	Arg	Ala	Leu	Arg	Met	Pro	Asn	Tyr	Lys	Lys	
		370				375					380					
Lys	Ala	Pro														
385																